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OM protein - protein search, using sw model

Run on: September 26, 2000, 19:26:58 ; search time 10.93 Seconds
(without alignments)
239.825 Million cell updates/sec

Title: Perfect score:
Sequence: US-09-218-277-12
Scoring table: ORIGO_Gapop 60.0 , Gapext 60.0

Searched: 152396 seqs, 15329161 residues

Word size : 0

Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents_AA:*

1: /cgnl-7/pctdata/1/1aa/5A_COMB.pep:*

2: /cgnl-7/podata/1/1aa/5B_COMB.pep:*

3: /cgnl-7/podata/1/1aa/6_COMB.pep:*

4: /cgnl-7/podata/1/1aa/pctus_COMB.pep:*

5: /cgnl-7/podata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result NO. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------------|--------------------|
| 1 | 171 | 100.0 | 171 | 2 | US-08-781-122-2 |
| 2 | 170 | 99.4 | 170 | 2 | US-08-227-357A-1 |
| 3 | 63 | 36.8 | 5 | 5194425 | Patent No. 5194425 |
| 4 | 41 | 24.0 | 170 | 1 | US-08-227-372-1 |
| 5 | 41 | 24.0 | 170 | 3 | US-08-170-397-1 |
| 6 | 41 | 24.0 | 170 | 5 | 5194425 |
| 7 | 40 | 23.4 | 40 | 3 | US-08-297-395-2 |
| 8 | 15.2 | 170 | 5 | 5468481 | |
| 9 | 24 | 24.0 | 15 | 2 | US-08-180-150-46 |
| 10 | 24 | 24.0 | 2 | US-08-188-319-46 | |
| 11 | 24 | 14.0 | 24 | 4 | PCT-US3-0745-46 |
| 12 | 23 | 23 | 1 | US-08-187-547-1 | |
| 13 | 21 | 12.3 | 21 | 1 | US-08-187-547-33 |
| 14 | 20 | 11.7 | 20 | 1 | US-08-227-372-4 |
| 15 | 20 | 11.7 | 20 | 1 | US-08-187-547-34 |
| 16 | 20 | 11.7 | 20 | 1 | US-08-187-547-35 |
| 17 | 20 | 11.7 | 20 | 1 | US-08-187-547-40 |
| 18 | 20 | 11.7 | 20 | 2 | US-08-160-344-6 |
| 19 | 20 | 11.7 | 20 | 2 | US-08-160-344-8 |
| 20 | 20 | 11.7 | 20 | 2 | US-08-168-540B-1 |
| 21 | 20 | 11.7 | 20 | 2 | US-08-168-540B-2 |
| 22 | 20 | 11.7 | 20 | 2 | US-08-168-540B-4 |
| 23 | 20 | 11.7 | 20 | 2 | US-08-168-540B-5 |
| 24 | 20 | 11.7 | 20 | 2 | US-08-168-540B-10 |
| 25 | 20 | 11.7 | 20 | 2 | US-08-168-540B-11 |
| 26 | 20 | 11.7 | 20 | 2 | US-08-168-540B-13 |
| 27 | 20 | 11.7 | 20 | 2 | US-08-606-630A-5 |
| 28 | 20 | 11.7 | 20 | 2 | US-08-606-630A-5 |

ALIGNMENTS

| RESULT | 1 |
|--|---|
| US-08-781-122-2 | ; Sequence 2, Appli |
| Patent No. 51948764 | GENERAL INFORMATION: |
| APPLICANT: Gaur, Amitabh | APPLICANT: Conlon, Paul J. |
| APPLICANT: Ling, Nicholas | TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS |
| NUMBER OF SEQUENCES: 2 | TITLE OF INVENTION: UTILIZING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC PROTEIN |
| CORRESPONDENCE ADDRESS: | ADDRESSEE: SEED and BERRY LLP |
| STREET: 6300 Columbia Center, 701 Fifth Avenue | CITY: Seattle |
| STATE: Washington | STATE: Washington |
| ZIP: 98104-1092 | ZIP: 98104-1092 |
| COMPUTER READABLE FORM: | |
| MEDIUM TYPE: Floppy disk | |
| COMPUTER: IBM PC compatible | |
| OPERATING SYSTEM: PC-DOS/MS-DOS | |
| SOFTWARE: Patent Release #1.0, Version #1.25 | |
| CURRENT APPLICATION DATA: | |
| APPLICATION NUMBER: US-08-781,122 | |
| FILING DATE: 09-JAN-1997 | |
| CLASSIFICATION: 514 | |
| ATTORNEY/AGENT INFORMATION: | |
| NAME: Mak, David J. | |
| NAME: Mak, David J. | |
| REGISTRATION NUMBER: 31,392 | |
| REFERENCE DOCKET NUMBER: 690068.418C1 | |
| TELECOMMUNICATION INFORMATION: | |
| TELEPHONE: (206) 622-4900 | |
| TELEFAX: (206) 622-6031 | |
| INFORMATION FOR SEQ ID NO: 2: | |
| SEQUENCE CHARACTERISTICS: | |
| LENGTH: 171 amino acids | |
| TYPE: amino acid | |
| TOPOLOGY: linear | |
| MOLECULE TYPE: protein | |
| ; Query Match | |
| Best Local Similarity 100.0%; Score 171; DB 2; Length 171; | |
| Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Qy | 1 MASQKPSQRGSKYIATASTMDHARRGFLPRHRDTGILDSIGRFFGGRGAKRGSGKD 60 |
| Db | 1 MASQKPSQRGSKYIATASTMDHARRGFLPRHRDTGILDSIGRFFGGRGAKRGSGKD 60 |

QY 61 SHHPARTAHGSLPKSHGRTODENPVVHFKNITVTPRTPPSOCKRGRLSLSRSWGAEG 120
 Db 61 SHHPARTAHGSLPKSHGRTODENPVVHFKNITVTPRTPPSOCKRGRLSLSRSWGAEG 120
 QY 121 GORPFGYGGGRASDYKSAHKGFKGVDQGTLSKIFKLGGDRSSPMARR 171
 Db 121 GORPFGYGGGRASDYKSAHKGFKGVDQGTLSKIFKLGGDRSSPMARR 171

RESULT 2
 US-08-327-357A-1
 Sequence 1, Application US/08327357A
 Patent No. 5817629
 GENERAL INFORMATION:
 APPLICANT: WARREN, Kenneth G.
 ADDRESS: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/327,357A
 FILING DATE: 21-OCT-1994
 CLASSIFICATION: 514
 PRIORITY DATA:
 APPLICATION NUMBER: CA 2,053,799-0
 FILING DATE: 22-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Innen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 27052-115469
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-952-4810
 TELEFAX: 202-962-8300
 INFORMATION FOR SBO ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: human myelin basic protein
 US-08-327-357A-1

RESULT 2
 US-08-327-357A-1
 Sequence 1, Application US/08327357A
 Patent No. 5817629
 GENERAL INFORMATION:
 APPLICANT: CATZ, Ingrid
 ADDRESS: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/367,751
 FILING DATE: 21-JUN-1989
 PRIORITY DATA:
 APPLICATION NUMBER: 210,594
 FILING DATE: 23-JUN-1988
 SEQ ID NO: 4:
 LENGTH: 168
 5194425-4

RESULT 3
 US-08-227-372-1
 Sequence 1, Application US/08227372
 Patent No. 5763585

GENERAL INFORMATION:
 APPLICANT: NG, Bishwajit
 TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF
 TITLE OF INVENTION: MIC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: Steuart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/227,372
 FILING DATE: 14-APR-1994
 CLASSIFICATION: 424
 PRIORITY DATA:
 APPLICATION NUMBER: US/08/135,216
 FILING DATE: 13-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 14058-32-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..170
 OTHER INFORMATION: /note= "Myelin basic protein"
 US-08-227-372-1

RESULT 5
 US-08-470-397-1
 Sequence 1, Application US/08470397
 Patent No. 6007820
 GENERAL INFORMATION:
 APPLICANT: Nag, Bishwaliit
 TITLE OF INVENTION: Purification and Characterization of
 MHC-peptide Complexes Useful in Ameliorating Autoimmunity
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: One Market Plaza, Stewart Street Tower, 20th
 STREET: Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08470,397
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/136,216
 FILING DATE: 13-OCT-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 14058-32-1-1
 FILING DATE: 14-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 14058-32-1-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1

OTHER INFORMATION: /product= "OTHER"
 OTHER INFORMATION: /note= "Xaa = N-acetyl-alanine"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 3
 OTHER INFORMATION: /product= "OTHER"
 OTHER INFORMATION: /note= "Xaa = Ala or absent"
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 NAME/KEY: Modified-site
 LOCATION: 10
 OTHER INFORMATION: /product= "OTHER"
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 NAME/KEY: Modified-site
 LOCATION: 11
 OTHER INFORMATION: /product= "OTHER"
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 NAME/KEY: Modified-site
 LOCATION: 15
 OTHER INFORMATION: /product= "OTHER"
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 NAME/KEY: Modified-site
 LOCATION: 40
 OTHER INFORMATION: /product= "OTHER"
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 NAME/KEY: Modified-site
 LOCATION: 46
 OTHER INFORMATION: /product= "OTHER"
 OTHER INFORMATION: /note= "Xaa = Ser or Gly"
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 NAME/KEY: Modified-site
 LOCATION: 59
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 OTHER INFORMATION: /note= "Xaa = Gly or Ser"
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 NAME/KEY: Modified-site
 LOCATION: 66
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 NAME/KEY: Modified-site
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 NAME/KEY: Modified-site
 LOCATION: 80
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 LOCATION: 141
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 OTHER INFORMATION: /note= "Xaa = Ile or Val"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 144
 OTHER INFORMATION: /product= "OTHER"
 OTHER INFORMATION: /note= "Xaa = His or Val"
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..170
 OTHER INFORMATION: /note= "Myelin basic protein"
 US-08-470-397-1

Query Match

24.0%; Score 41; DB 3; Length 170;

Best Local Similarity 100.0%; Pred. No. 7.1e-33; Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SLPOKSHGRTQDENPVVHFFKNIVTPRTPPSQGKGRLS 40

RESULT

8

5468481-3

; Patent No. 5468481

; APPLICANT: SHARMA, SOMESH D.; CLARK, BRIAN R.

; TITLE OF INVENTION: MHC CLASS II-PEPTIDE CONJUGATES USEFUL

; IN AMELIORATING AUTOIMMUNITY

; NUMBER OF SEQUENCES: 9

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/869, 293

; FILING DATE: 14-APR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 690, 840

; FILING DATE: 23-APR-1991

; APPLICATION NUMBER: 576, 084

; FILING DATE: 30-AUG-1990

; APPLICATION NUMBER: 210, 594

; FILING DATE: 23-JUN-1989

; APPLICATION NUMBER: 635, 840

; FILING DATE: 28-DEC-1998

; APPLICATION NUMBER: 367, 751

; FILING DATE: 21-JUN-1989

; SEQ ID NO:3:

; LENGTH: 170

; 5468481-3

; RESULT

7

US-08-297-395-2

; Query Match 24.0%; Score 41; DB 5; Length 170; Best Local Similarity 100.0%; Pred. No. 7.1e-33; Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; GENERAL INFORMATION:

; Patent No. 633947

; APPLICANT: Howard L. Weiner

; APPLICANT: David A. Hafner

; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT

; TITLE OF INVENTION: EPTOPES OF MYELIN BASIC PROTEIN

; FILE REFERENCE: 1010-05723US3

; CURRENT APPLICATION NUMBER: US/08/297, 395A

; CURRENT FILING DATE: 1994-05-11

; EARLIER APPLICATION NUMBER: 08/059, 189

; EARLIER FILING DATE: 1993-05-06

; EARLIER APPLICATION NUMBER: 07/502, 559

; EARLIER FILING DATE: 1990-03-30

; EARLIER APPLICATION NUMBER: PCT/US88/02139

; EARLIER FILING DATE: 1988-06-24

; EARLIER APPLICATION NUMBER: 07/065, 734

; EARLIER FILING DATE: 1987-06-24

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: FASTSEQ for Windows version 3.0

; SEQ ID NO: 2

; LENGTH: 40

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-08-297-395-2

; RESULT

9

US-08-480-190-46

; Query Match 15.2%; Score 26; DB 5; Length 170; Best Local Similarity 100.0%; Pred. No. 3.4e-18; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; GENERAL INFORMATION:

; Patent No. 5827515

; APPLICANT: Robert G. Urban

; APPLICANT: Roman M. Chicz

; APPLICANT: Dario A. A. Vignali

; APPLICANT: Mary L. Hedley

; APPLICANT: Lawrence J. Stern

; APPLICANT: Jack L. Strominger

; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

; NUMBER OF SEQUENCES: 214

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 MB

; COMPUTER: IBM PS/2 Model 50Z or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/480, 190

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/077, 255

; FILING DATE: June 15, 1993

; APPLICATION NUMBER: 07/1925, 460

; FILING DATE: August 11, 1992

; ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30.162
 REFERENCE/DOCKET NUMBER: 00246/168001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS: 46:
 LENGTH: 24
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
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 US-08-480-190-46
 ;
 Query Match 14.0%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 79 GRTQDENPVHFEKNTVPRTPPP 102
 Db 1 GRTQDENPVHFEKNTVPRTPPP 24
 ;
 RESULT 10
 US-08-488-379-46
 ; Sequence 46, Application US/08488379
 ; Patent No. 5880103
 GENERAL INFORMATION:
 APPLICANT: Robert G. Urban
 APPLICANT: Roman M. Chicz
 APPLICANT: Dario A. A. Vignali
 APPLICANT: Mary L. Hedley
 APPLICANT: Lawrence J. Stern
 APPLICANT: Jack L. Strominger
 TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
 NUMBER OF SEQUENCES: 273
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 COMPUTER: IBM PS/2 Model 50Z or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: Wordperfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/07545
 FILING DATE: 19930811
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/925,460
 FILING DATE: August 11, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30.162
 REFERENCE/DOCKET NUMBER: 00246/168001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS: 46:
 LENGTH: 24
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 ;
 PCT-US93-07545-46
 ;
 Query Match 14.0%; Score 24; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 79 GRTQDENPVHFEKNTVPRTPPP 102
 Db 1 GRTQDENPVHFEKNTVPRTPPP 24
 ;
 RESULT 11
 PCT-US93-07545-46
 ; Sequence 46, Application PC/US9307545
 ; GENERAL INFORMATION:
 APPLICANT: Robert G. Urban
 APPLICANT: Roman M. Chicz
 APPLICANT: Dario A. A. Vignali
 APPLICANT: Mary L. Hedley
 APPLICANT: Lawrence J. Stern
 TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
 NUMBER OF SEQUENCES: 273
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 COMPUTER TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 50Z or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: Wordperfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/07545
 FILING DATE: 19930811
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/925,460
 FILING DATE: August 11, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30.162
 REFERENCE/DOCKET NUMBER: 00246/168001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS: 46:
 LENGTH: 24
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 ;
 PCT-US93-07545-46
 ;
 Query Match 14.0%; Score 24; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 79 GRTQDENPVHFEKNTVPRTPPP 102
 Db 1 GRTQDENPVHFEKNTVPRTPPP 24
 ;
 RESULT 12
 US-08-87-547-1
 ; Sequence 1, Application US/08787547
 ; Patent No. 5783567

GENERAL INFORMATION:

APPLICANT: Hedley, Mary Lynne

APPLICANT: Curley, Joanne M.

APPLICANT: Langer, Robert S.

TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/787,547

FILING DATE: 22-JAN-1997

CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 14058-32-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Curley, Joanne M.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Hedley, Mary Lynne

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Curley, Joanne M.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Langer, Robert S.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Curley, Joanne M.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Hedley, Mary Lynne

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Curley, Joanne M.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Langer, Robert S.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Curley, Joanne M.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Curley, Joanne M.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Curley, Joanne M.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Peptide

US-08-787-547-33

Search completed: September 26, 2000, 19:36:55
 Job time: 597 sec

TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-227-372-4

Query Match 11.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e-13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

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|----|-----|----------------------|-----|
| Qy | 125 | GRGYGRASDYSKSAHGFKG | 144 |
| Db | 1 | GRGYGGRASDYSKSAHGFKG | 20 |

RESULT 15
 US-08-787-547-34
 Sequence 34, Application US/08787547
 Patent No. 5,83567
 GENERAL INFORMATION:
 APPLICANT: Hedley, Mary Lynne
 APPLICANT: Curley, Joanne M.
 APPLICANT: Langer, Robert S.
 TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
 TITLE OF INVENTION: OF NUCLEIC ACID
 NUMBER OF SEQUENCES: 107
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 COMPUTER: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/787,547
 FILING DATE: 22-JAN-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 08191/003001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEX: 617-542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-787-547-34

Query Match 11.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e-13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

| | | | |
|----|----|--------------------|----|
| Qy | 34 | RDGIGLDSIGRFGGDGAP | 53 |
| Db | 1 | RDGIGLDSIGRFGGDGAP | 20 |

Wed Sep 27 09:09:32 2000

us-09-218-277-12.rai

| | | | | | | | | | | |
|--|------------------|--|---|---|---|--------------------------|---|---|--|--|
| Copyright (c) 1993 - 2000 Comigen Ltd. | | | | | | | | | | |
| GenCore Version 4.5 | | | | | | | | | | |
| Run on: September 26, 2000, 19:26:53 ; Search time 11.86 Seconds | | | | | | | | | | |
| OM protein - protein search, using sw model | | | | | | | | | | |
| Scoring table: OLIGO | US-09-218-277-12 | Perfect score: 17.1 | Sequence: 1 MASQKPSQRIGSKYLATAS.....SKIFLKGGRDRDSRGSPMARR 171 | Word size : 0 | Total number of hits satisfying chosen parameters: 188963 | Minimum DB seq length: 0 | Maximum DB seq length: 200000000 | (without alignments) 341.511 Million cell updates/sec | | |
| Post-processing: Listing first 45 summaries | A_Genesed_36:* | Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | | | | |
| SUMMARIES | | | | | | | | | | |
| Result No. | Score | Query Match | Length | DB ID | Description | RESULT | 1 | ALIGNMENTS | | |
| 1 | 171 | 100.0 | 171 | 1 R87627 | Human myelin basic protein | R87627 | | | | |
| 2 | 171 | 100.0 | 171 | 1 R89580 | Human myelin basic protein | R87627 | standard; Protein; 171 AA. | | | |
| 3 | 170 | 99.4 | 170 | 1 R88592 | Human myelin basic protein | R87627; | | | | |
| 4 | 170 | 99.4 | 170 | 1 R85406 | Human myelin basic protein | DT | | | | |
| 5 | 113 | 66.1 | 197 | 1 W09399 | Human myelin basic protein | 03-NOV-1996 | (first entry) | | | |
| 6 | 113 | 66.1 | 203 | 1 W06107 | Human myelin basic protein | DE | | | | |
| 7 | 113 | 66.1 | 203 | 1 W06108 | Human myelin basic protein | KW | | | | |
| 8 | 113 | 66.1 | 373 | 1 W06103 | Human myelin basic protein | prevention; analogue. | | | | |
| 9 | 113 | 66.1 | 375 | 1 W06104 | Human myelin basic protein | OS | Homo sapiens. | | | |
| 10 | 113 | 66.1 | 385 | 1 W06102 | Human myelin basic protein | FH | location/Qualifiers | | | |
| 11 | 92 | 53.8 | 170 | 1 R8073 | Peptide analogue of human myelin basic protein | Key | | | | |
| 12 | 86 | 50.3 | 170 | 1 R35440 | Peptide analogue of human myelin basic protein | peptide | 86..99 | | | |
| 13 | 63 | 36.8 | 168 | 1 R04717 | Peptide analogue of human myelin basic protein | FT | /label= | claimed peptide region. | | |
| 14 | 46 | 26.9 | 1 W72360 | 1 MASQKPSQRIGSKYLATAS.....SKIFLKGGRDRDSRGSPMARR 171 | Peptide analogue of human myelin basic protein | PR | 16-NOV-1995 | U14402. | | |
| 15 | 46 | 26.9 | 171 | R88595 | Peptide analogue of human myelin basic protein | PA | 18-NOV-1994 | US-342078. | | |
| 16 | 46 | 26.9 | 171 | R88596 | Peptide analogue of human myelin basic protein | PA | (NEUR-) NEUROCRINE BIOSCIENCES INC. | | | |
| 17 | 45 | 26.3 | 168 | 1 R88594 | Peptide analogue of human myelin basic protein | PA | (SFRD) UNIV STANFORD MEDICAL CNT. | | | |
| 18 | 45 | 26.3 | 170 | 1 R02226 | Peptide analogue of human myelin basic protein | PI | Conlon PJ, Gaur A, Ling N, Steinman L; | | | |
| 19 | 41 | 24.0 | 170 | 1 R0735 | Peptide analogue of human myelin basic protein | DR | WPI; 96-268534/27. | | | |
| 20 | 41 | 24.0 | 170 | 1 R5947 | Peptide analogue of human myelin basic protein | DR | N_PSDB; T30269. | | | |
| 21 | 41 | 24.0 | 170 | 1 R5947 | Peptide analogue of human myelin basic protein | PT | Peptide analogue of human myelin basic protein - has Lysine 91 replaced by another amino acid, useful to treat multiple sclerosis | | | |
| 22 | 41 | 24.0 | 170 | 1 R88593 | Peptide analogue of human myelin basic protein | PS | Claim 1; Figure 1; 30pp; English. | | | |
| 23 | 33 | 19.3 | 169 | 1 R85135 | Peptide analogue of human myelin basic protein | CC | A peptide analogue comprising amino acids 87-99 of human myelin basic protein (MBP), where Lys91 is substituted for another amino acid can be used to treat and prevent multiple sclerosis. The peptide analogue is administered at a dosage range of 5-50 mg/kg. | | | |
| 24 | 32 | 18.7 | 32 | 1 R85369 | Peptide analogue of human myelin basic protein | CC | acid can be used to treat and prevent multiple sclerosis. The peptide analogue is administered at a dosage range of 5-50 mg/kg. | | | |
| 25 | 32 | 18.7 | 32 | 1 R85369 | Peptide analogue of human myelin basic protein | SQ | Sequence 171 AA; | | | |
| 26 | 27 | 15.8 | 27 | R85372 | Peptide analogue of human myelin basic protein | Query | Best Local Similarity 100.0%; Score 171; DB 1; Length 171; Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| 27 | 26 | 15.2 | 170 | 1 R86422 | Peptide analogue of human myelin basic protein | Match | | | | |
| 28 | 25 | 14.6 | 25 | 1 R85135 | Peptide analogue of human myelin basic protein | RESULT | 1 | | | |
| 29 | 25 | 14.6 | 25 | 1 R85371 | Peptide analogue of human myelin basic protein | ID | R89580 standard; Protein; 171 AA. | | | |
| 30 | 25 | 14.6 | 25 | 1 R85367 | Peptide analogue of human myelin basic protein | AC | R89580; | | | |
| 31 | 25 | 14.6 | 25 | 1 R85342 | Peptide analogue of human myelin basic protein | DT | 07-NOV-1996 (first entry) | | | |
| 32 | 25 | 14.6 | 25 | 1 R85346 | Peptide analogue of human myelin basic protein | DE | Human myelin basic protein (MBP). | | | |
| 33 | 25 | 14.6 | 25 | 1 R95347 | Peptide analogue of human myelin basic protein | KW | Myelin basic protein; MBP; multiple sclerosis; MS; competition; inhibition; major histocompatibility complex; MHC; thymocyte; T cell; | | | |

| | |
|-----------------------|--|
| KW | experimental allergic encephalomyelitis; EAE; analogue. |
| OS | homo sapiens. |
| PN | WQ9616086-A1. |
| PR | 30-MAY-1995; U14403; |
| PF | 16-NOV-1995; U14403; |
| PR | 18-NOV-1994; US-342408. |
| PA | (NEUR-) NEUROCRINE BIOSCIENCES INC. |
| PI | Conlon PJ, Gaur A, Ling N, Steinman L; |
| DR | WTI; 96-2-68535/27. |
| DR | DR-PSDB; T32561. |
| PT | Peptide analogues of human myelin basic protein - useful for treatment of multiple sclerosis. |
| PS | Disclosure; Figure 1; 61PP; English. |
| CC | Peptide analogues comprising at least seven amino acids from residues 86-99 of human myelin basic protein (MBP), can be used to treat multiple sclerosis by competing for the binding of native MBP peptide to MHC and by not causing proliferation of an MBP reactive T-cell line. The peptide analogues also inhibit the induction of experimental allergic encephalomyelitis (EAE) by MBP in rodents. |
| CC | The peptide analogues have a reduced susceptibility to proteolysis in vivo. |
| CC | Sequence 171 AA: |
| Query Match | 100.0%; Score 171; DB 1; Length 171; |
| Best Local Similarity | 100.0%; Pred. No. 5 7e-161; |
| Matches | 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 ASOKRPSQRGSKYLTASTMDHARHGFLPRHRDGLDSIGREFGGDGAPKRGSGKDS 61 |
| Db | 1 ASOKRPSQRGSKYLTASTMDHARHGFLPRHRDGLDSIGREFGGDGAPKRGSGKDS 61 |
| Qy | 2 ASOKRPSQRGSKYLTASTMDHARHGFLPRHRDGLDSIGREFGGDGAPKRGSGKDS 61 |
| Db | 1 ASOKRPSQRGSKYLTASTMDHARHGFLPRHRDGLDSIGREFGGDGAPKRGSGKDS 61 |
| Qy | 62 HHPARTAHGSILPKSHGRTDENPVVFHKNTVPRTPPSQOKGRGSLSRSSWAGC 121 |
| Db | 61 HHPARTAHGSILPKSHGRTDENPVVFHKNTVPRTPPSQOKGRGSLSRSSWAGC 120 |
| Qy | 122 QRPGEYGGGRASDYKSAHKGFKGVDAGTSLKFKLGGDRSRSGPMMARR 171 |
| Db | 121 ORPGFQYGGGRASDYKSAHKGFKGVDAGTSLKFKLGGDRSRSGPMMARR 170 |
| RESULT | 4 |
| ID | R95406 |
| AC | R95406 standard; Protein: 170 AA. |
| DT | 16-DEC-1996 (first entry) |
| DE | Myelin oligodendrocyte protein. |
| KW | Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE; CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG; relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP; diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome; KW psoriasis; thyroiditis; rheumatoid arthritis; Proteolipid protein; MAG; myelin oligodendrocyte protein; myelin associated glycoprotein; therapy. |
| OS | homo sapiens. |
| PN | WQ9616086-A2. |
| PD | 02-MAY-1995. |
| PP | 25-OCT-1995; U133682. |
| PR | 25-OCT-1994; US-328224. |
| PR | 15-MAR-1995; US-404228. |
| PR | 25-OCT-1995; ZA-009033. |
| PA | (IMMU-) IMMUNOLOGIC PHARM CORP. |
| PI | Devaux B, Franzen H, Gitter M, Hsu D, Paliard X; |
| PI | Rothbard J, Samson M, Shi J, Smilie D; |
| DR | WPI; 96-230552/23. |
| PT | Myelin basic derived peptide(s) and analogs - used in the treatment of Multiple Sclerosis, Psoriasis, Graves Disease, etc. |
| PS | Example 9; Fig 1; 91PP; English. |
| CC | This sequence represents the human myelin oligodendrocyte protein (MOG). Immunisation with MOG (or the peptide fragments shown in R95375/R95385) can be used to induce experimental allergic encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+ T-cell mediated autoimmune disease which results in demyelination of the central nervous system, resulting in paralysis and other neurological abnormalities. EAE is a commonly used animal model for human multiple sclerosis (MS). These sequences can be used in compositions for treating MS in a mammal. The composition acts to down regulate the autoimmune response, and may be administered in an amount sufficient to prevent the onset of symptoms of MS. The compositions may also be used to treat advanced stage MS, especially relapsing-remitting MS, chronic progressive MS or benign MS. These peptides may also be used in the treatment of other diseases involving myelin autoantigens, including diabetes, Graves disease, myasthenia gravis, Good Pasture's syndrome, psoriasis, thyroiditis, and rheumatoid arthritis. Peptides derived from other myelin autoantigens, such as myelin basic protein (MBP, see R9534-R9537), proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can be used as alternatives to the MOG peptides in these compositions. |
| SQ | Sequence 170 AA; |
| Query Match | 99.4%; Score 170; DB 1; length 170; |
| Best Local Similarity | 100.0%; Pred. No. 5.5e-160; |
| Matches | 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 2 ASOKRPSQRGSKYLTASTMDHARHGFLPRHRDGLDSIGREFGGDGAPKRGSGKDS 61 |
| Db | 1 ASOKRPSQRGSKYLTASTMDHARHGFLPRHRDGLDSIGREFGGDGAPKRGSGKDS 60 |

Query Match 99.4%; Score 170; DB 1; Length 170;

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| PR | /label= "Epitope | /note= "PIP epitope associated with MS" |
| PR | /note= "PIP epitope associated with MS" | 248. .269 |
| FT | region | /label= "Epitope |
| FT | region | /note= "PIP epitope associated with MS" |
| FT | region | 256. .269 |
| FT | region | /label= "Epitope |
| FT | region | /note= "PIP epitope associated with MS" |
| FT | region | 257. .269 |
| FT | region | /label= "Epitope |
| FT | region | /note= "PIP epitope associated with MS" |
| FT | region | 268. .281 |
| FT | region | /label= "Epitope |
| FT | region | /note= "PIP epitope associated with MS" |
| FT | region | 270. .303 |
| FT | region | /label= "Epitope |
| FT | region | /note= "PIP epitope associated with MS" |
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| FT | region | /label= "Epitope |
| FT | region | /note= "PIP epitope associated with MS" |
| FT | region | 292. .307 |
| FT | region | /label= "Epitope |
| FT | region | /note= "PIP epitope associated with MS" |
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| FT | region | /note= "PIP epitope associated with MS" |
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| FT | region | /note= "PIP epitope associated with MS" |
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| FT | region | /note= "PIP epitope associated with MS" |
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| FT | region | /note= "PIP epitope associated with MS" |
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| FT | region | /note= "encephalitogenic epitope in mouse model" |
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| FT | region | 292. .304 |
| FT | region | /label= "Epitope |
| FT | peptide | /note= "encephalitogenic epitope associated with MS" |
| FT | peptide | 369. .373 |
| FT | peptide | /label= "Histidine-tag |
| FT | peptide | /note= "hoxa-histidine-tag protein purification" |
| FT | peptide | W09634622-A1. |
| PN | W09634622-A1. | |
| PD | 07-NOV-1996. | |
| PR | 22-APR-1995; U05611. | |
| PR | 02-MAR-1995; US-431144. | |
| PR | 02-MAY-1995; US-431144. | |
| PR | 07-JUN-1995; US-482114. | |
| PA | (ALEX-) ALEXION PHARM INC. | |
| PA | (USSH) US DEPT HEALTH & HUMAN SERVICES. | |
| PI | Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP; | |
| PI | Nye SR, Pelfrey CM, Squinto SP, Wilkins JA; | |
| DR | WPI: 96-505898/50. | |
| DR | N-PSDB; T1893. | |
| PT | New human myelin basic protein and proteolipid protein variant(s) - | |
| PT | used in the assessment, diagnosis and treatment of multiple | |
| PT | sclerosis | |
| PS | Claim 34; Page 110-112; 156PP; English. | |
| CC | MP4 chimeria (W06103) is a fusion protein composed of human myelin | |
| CC | basic protein (MBP) foetal isoform MBP1.5 (see also W00399) and | |
| CC | delta PIP4 (W06101), a proteolipid protein (PIP) mutant that lacks | |
| CC | all 4 hydrophobic domains of native human PIP (W06106) but | |
| CC | includes PIP epitopes associated with multiple sclerosis (MS). It | |
| CC | includes PIP epitopes associated with multiple sclerosis (MS). It | |

CC can be expressed in *E. coli* transformants using a DNA construct (T41893) contg. the MBP21.5-delta PLP4 gene fusion. MP4 chimera and other novel PLP/MBP21.5 PolyPeptides (W00399-400, W06101-08) are useful for the clinical assessment, diagnosis and treatment of MS.

SQ Sequence 373 AA:

Query Match 66.1%; Score 113; DB 1; Length 373;
Best Local Similarity 100.0%; Pred. No. 1.3e-103; Indels 0; Gaps 0;
Matches 113; Conservative 0; Mismatches 0; region 113-.373

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FT /note= "PLP epitope associated with MS"
FT region 115-.127
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FT /note= "PLP epitope associated with MS"
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FT region 127-.140
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT region 152-.166
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT region 144
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT region 14-.35
FT /label= Epitope
FT /note= "encephalitogenic epitope in mouse model"
FT region 57-.70
FT /label= Epitope
FT /note= "encephalitogenic epitope in mouse model"
FT region 93-.105
FT /label= Epitope
FT /note= "encephalitogenic epitope in mouse model"
FT peptide 170-.173
FT /label= Spacer
FT domain 174-.368
FT /label= MBP21.5
FT peptide 369-.375
FT /label= Histidine-tag
FT /note= "hexa-histidine tag facilitates recombinant protein purification"

FT PN w09634622-A1.
FT PD 07-NOV-1996.
FT PF 22-APR-1996; US-6111.
FT PR 02-MAY-1995; US-431648.
FT PR 02-MAY-1995; US-431644.
FT PR 07-JUN-1995; US-482114.
FT PA (ALEX-) ALEXION PHARM INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Lenardo MJ, Mattis L, McCarland HF, Mueller EE, Mueller JP;
PI Nye SH, Peltrey CM, Squinto SP, Wilkins JA;
DR WI; 96-50598/50.
DR NPDB; T41894.

PT New human myelin basic protein and proteolipid protein variant(s) - used in the assessment, diagnosis and treatment of multiple sclerosis

PS Claim 35; Page 113-114; 16pp; English.

CC PM4 chimera (W06104) is a fusion protein composed of delta PLP4 (W06101) and MBP21.5 (W00399). Delta PLP4 is a proteolipid protein (PLP) myelin that lacks all 4 hydrophobic domains of native human PLP (W06106) but includes PLP epitopes associated with multiple sclerosis (MS). MBP21.5 is a foetal isoform of human myelin basic protein (MBP), associated with MS. PLP is in reverse orientation to MB4 chimera (W06103). It can be expressed in bacterial host cells using a DNA construct (T41893). PLP polypeptides (see also W00400, W06101-03 and W06105) can be used in the clinical assessment, diagnosis and treatment of MS.

SQ Sequence 375 AA:

Query Match 66.1%; Score 113; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-103; Indels 0; Gaps 0;
Matches 113; Conservative 0; Mismatches 0; region 113-.375

FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT region 96-.107
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT region 115-.127
FT /label= Epitope
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FT region 152-.166
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FT region 14-.35
FT /label= Epitope
FT /note= "encephalitogenic epitope in mouse model"
FT region 57-.70
FT /label= Epitope
FT /note= "encephalitogenic epitope in mouse model"
FT region 93-.105
FT /label= Epitope
FT /note= "encephalitogenic epitope in mouse model"
FT peptide 170-.173
FT /label= Spacer
FT domain 174-.368
FT /label= MBP21.5
FT peptide 369-.375
FT /label= Histidine-tag
FT /note= "hexa-histidine tag facilitates recombinant protein purification"

FT PN w09634622-A1.
FT PD 07-NOV-1996.
FT PF 22-APR-1996; US-6111.
FT PR 02-MAY-1995; US-431648.
FT PR 02-MAY-1995; US-431644.
FT PR 07-JUN-1995; US-482114.
FT PA (ALEX-) ALEXION PHARM INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Lenardo MJ, Mattis L, McCarland HF, Mueller EE, Mueller JP;
PI Nye SH, Peltrey CM, Squinto SP, Wilkins JA;
DR WI; 96-50598/50.
DR NPDB; T41894.

PT New human myelin basic protein and proteolipid protein variant(s) - used in the assessment, diagnosis and treatment of multiple sclerosis

PS Claim 35; Page 113-114; 16pp; English.

CC PM4 chimera (W06104) is a fusion protein composed of delta PLP4 (W06101) and MBP21.5 (W00399). Delta PLP4 is a proteolipid protein (PLP) myelin that lacks all 4 hydrophobic domains of native human PLP (W06106) but includes PLP epitopes associated with multiple sclerosis (MS). MBP21.5 is a foetal isoform of human myelin basic protein (MBP), associated with MS. PLP is in reverse orientation to MB4 chimera (W06103). It can be expressed in bacterial host cells using a DNA construct (T41893). PLP polypeptides (see also W00400, W06101-03 and W06105) can be used in the clinical assessment, diagnosis and treatment of MS.

SQ Sequence 375 AA:

| Db | 317 AEGQPGFGYGRASDYKSAHKGFKGVDAQTLISKIFKLGGDRSSGSPMARR 369 | Key |
|--------|--|--|
| RESULT | 10 | Location/Qualifiers |
| ID | W06102 | 1. .487 |
| AC | W06102; standard; Protein; 385 AA. | /note= "preferred protein of the invention" |
| DT | 01-FEB-1997 (first entry) | 1. .197 |
| DE | MP3 chimera (MBP21.5-delta PLP3 fusion). | /label= MBP21.5 |
| KW | Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP; | /label= MOG |
| KW | MBP21.5; multiple sclerosis; autoimmune disease; diagnosis; | /note= "MOG extracellular domain" |
| KW | therapy; T-lymphocyte; T-cell; myelin basic protein; diagnosis; OS | /label= Delta_PLP4 |
| OS | Synthetic. | /label= MBP21.5 |
| FH | Location/Qualifiers | 198 - 319 |
| FT | domain | /label= MBP21.5 |
| FT | domain | 320 - 406 |
| FT | domain | 327 - 338 |
| FT | region | 360 - 380 |
| FT | region | 363 - 376 |
| FT | region | 367 - 378 |
| FT | region | 375 - 388 |
| FT | region | 376 - 388 |
| FT | region | 387 - 400 |
| FT | region | 389 - 402 |
| FT | region | 411 - 423 |
| FT | region | 414 - 425 |
| FT | region | 433 - 445 |
| FT | region | 445 - 456 |
| FT | region | 445 - 458 |
| FT | region | 470 - 484 |
| FT | region | 332 - 353 |
| FT | region | 375 - 388 |
| FT | region | 411 - 423 |
| FT | region | 487 - 492 |
| FT | peptide | /label= Histidine-tag |
| FT | peptide | /note= "hexa-histidine tag facilitates recombinant |
| FT | peptide | |
| RESULT | 11 | |
| ID | W06105 | |
| AC | W06105; standard; Protein; 492 AA. | |
| DT | 01-FEB-1997 (first entry) | |
| DE | MMOG4 chimera (MBP21.5-MOG-delta PLP4 fusion). | |
| KW | Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP; | |
| KW | MBP21.5; multiple sclerosis; autoimmune disease; diagnosis; | |
| KW | therapy; T-lymphocyte; T-cell; Mmog4 chimera; | |
| KW | myelin oligodendrocyte glycoprotein; MOG. | |
| OS | Synthetic. | |

| | | |
|--------|---|--|
| FT | W09634622-A1. | protein purification" |
| PD | 07-NOV-1996 | 53.8%; Score 92; DB 1; Length 170; |
| PF | 22-APR-1996; US05611 | Best Local Similarity 100.0%; Pred. No. 3.3e-83; Mismatches 0; Indels 0; Gaps 0; Matches 92; |
| PR | 02-MAY-1995; US431648 | Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| PR | 07-JUN-1995; US 482114 | |
| PA | (ALEX-) ALEXION PHARM INC. | |
| PA | (USSH) US DEPT HEALTH & HUMAN SERVICES. | |
| PA | Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP; | |
| PI | Nye SH, Palfrey CM, Squinto SP, Wilkins JA; | |
| DR | WPI: 96-50898/50. | |
| DR | N-PSPDB: T41895. | |
| PT | New human myelin basic protein and proteolipid protein variant(s) - | |
| PT | used in the assessment, diagnosis and treatment of multiple | |
| PT | sclerosis | |
| PS | Claim 36; Page 115-117; 156pp; English. | |
| ID | MNQGP4 chimera (W05105) is a fusion protein composed of human myelin basic protein (MBP) foetal isofrom MBP21.5 (see also W00599), the extracellular domain of human myelin oligodendrocyte glycoprotein (MOG) and delta PLP4 (W05101), a proteolipid protein (PLP) mutant. MBP21.5, PLP and MOG are all recognised by autoreactive T cells from multiple sclerosis (MS) patients. The chimera was produced using a DNA construct (T41895) obt'd. by inserting a sequence encoding the MOG moiety into MP4 chimera DNA (see also T41893). MNQGP4 chimera can be expressed in bacterial cell hosts. PLP and MBP polypeptides (see also W00400, W05101-04, W05107-08) are useful in the clinical assessment, diagnosis and treatment of MS. | |
| SQ | Sequence 492 AA; | |
| RESULT | 12 | |
| R30736 | R30736 standard; Protein; 170 AA. | RESULT 13 |
| ID | R30736; Standard; Protein; 170 AA. | R35440 |
| AC | R35440; standard; protein; 170 AA. | ID R35440 |
| DT | 13-AUG-1993 (first entry) | AC R35440; |
| DE | Human basic myelin protein. | DT 13-AUG-1993 |
| KW | MBP; MS; multiple sclerosis; homologue; myelin basic protein; MBP. | DE Human basic myelin protein. |
| OS | Homo sapiens. | KW |
| FR | Key peptide 61..106 | OS Homo sapiens. |
| FT | /note= "neutralising fragment" | FR Key |
| FT | 1..15 | FT peptide |
| FT | /note= "neutralising fragment" | FT peptide |
| FT | 4..18 | FT peptide |
| FT | /note= "neutralising fragment" | FT peptide |
| FT | 9..23 | FT peptide |
| FT | /note= "neutralising fragment" | FT peptide |
| FT | 15..35 | FT peptide |
| FT | /note= "neutralising fragment" | FT peptide |
| FT | 20..37 | FT peptide |
| FT | /note= "neutralising fragment" | FT peptide |
| FT | 31..46 | FT peptide |
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| FT | /note= "acylated" | FT modified_site |
| PN | W09308212-A. | FT modified_site |
| PD | 29-APR-1993. | FT modified_site |
| PF | 15-OCT-1992; CA0448. | FT modified_site |
| PR | 22-OCT-1991; CA-053799. | FT modified_site |
| PA | (CATZ/) CATZ I. | FT modified_site |
| PA | (WARR/) WARREN K G. | FT modified_site |
| PI | Catz I, Warren KG, | FT modified_site |
| DR | WPI: 93-152422/18. | FT modified_site |
| DE | Human MBP. | FT modified_site |
| KW | Acetylcholine receptor; MHC; myelin basic protein; MBP. | FT modified_site |
| OS | Synthetic. | FT modified_site |
| FT | Key location/Qualifiers | FT modified_site |
| FT | modified_site 1 | FT modified_site |
| FT | /note= "N-Ac-Ala" | FT modified_site |
| FT | modified_site 107 | FT modified_site |
| FT | /note= "Me-Arg" | FT modified_site |
| FT | peptide 1..14 | FT modified_site |
| FT | /note= "claim 30; page 68" | FT modified_site |
| PN | W09218150-A. | FT modified_site |
| PD | 29-OCT-1992. | FT modified_site |
| PF | 23-APR-1992; US03391 | Query Match |
| PR | 23-APR-1991; US 690840. | Best Local Similarity 100.0%; Pred. No. 2.7e-77; Mismatches 0; Indels 0; Gaps 0; Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| PA | (ANER-) ANERGEN INC. | |
| PI | Clark BR, Larch BL, Sharma SD; | |
| DR | WPI: 93-036056/04. | |
| PR | pure major MHC-peptide complex - useful in treating deleterious immune response such as auto-immunity | |
| PS | Claim 30, Page 68 + Fig 7; 93pp; English. | |
| CC | A method is claimed for the prepn. of a pure major MHC-peptide complex. The MHC component is a Class II glycoprotein of the MHC and the peptide comprises amino acids 1-14 of MBP. | |
| CC | Sequence 170 AA; | |
| SQ | | |

RESULT 14
 ID R04717 standard; protein; 168 AA.
 AC R04717;
 DT 23-AUG-1990 (first entry)
 DE Empirically determined sequence of myelin basic Protein (MBP)
 KW Myelin basic protein; multiple sclerosis; autoantigen; autoimmune disease;
 KW epitope; myelin sheath.
 KW key location/qualifiers
 FT misc_difference 1
 FT /label=OTHER
 FT /note="N-Ac-Ala"
 FT 168 /label=OTHER
 FT /note="Arg-COOH"
 PN W08912459-A.
 PD 28-DEC-1989.
 PR 23-JUN-1989; US-367751; US-210594.
 PA (BIOS-) Biospan Corp.
 PI Sharma SD, Larch LB, Clark BR;
 DR WPI: 90-022384/03.
 PT New complexes of histo-compatible glyco:protein -
 PT with antigenic peptide(s) and label or toxin, used to target
 PT antigen specific T helper cells
 PS Fig 7.; 7PP; English.
 CC The patient claims complexes of formulae (I), (II) and (III) which are as follows: (I) X - MHC - peptide; (II) MHC - peptide - X; (III) MHC - peptide where X = toxin or labelling gp.; MHC - effective portion of the major histocompatibility glycoprotein; and the peptide includes an epitope associated with one of the major autoimmune diseases, including multiple sclerosis (MS). MBP is the principle autoantigen in MS and is a candidate peptide for insertion in the complexes which can be used to treat and monitor MS. Pertinent sections of MBP are determined empirically using a strain of mice which develops experimental allergic encephalitis when immunised with bovine MBP. The sequence given in p94717 is with the substitution of the residues above the sequence in Fig 7. The sequence without substitutions is given in p9226.
 SQ 168 AA;

Query Match 36.8%; Score 63; DB 1; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.2e-54;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 GLSLSRFSWAGRGQRPGFGYGRASDVKSAHKGFKGVDAGTTLISKIFKLGSRDSRGSPM 168
 Db 106 GLSLSRFSWAGRGQRPGFGYGRASDVKSAHKGFKGVDAGTTLISKIFKLGSRDSRGSPM 165
 Qy 169 ARR 171
 |||
 Db 166 ARR 168

RESULT 15
 ID W72360
 ID W72360 standard; peptide; 46 AA.
 AC W72360;
 DT 16-DEC-1998 (first entry)
 DE Human myelin basic protein fragment.
 KW Human; myelin basic protein; MBP; multiple sclerosis; anti-MBP; MS.
 OS Homo sapiens.
 PN W09845327-A1.
 PD 15-OCT-1998.
 PR 03-APR-1998; CA0290;
 PR 04-APR-1997; CA-201841.
 PA (UVAL-) UNIV ALBERTA.
 PI Catz I, Warren KG;
 DR WPI; 98-563354/8.
 PT peptide and its derivatives for treatment of multiple sclerosis - is
 PT capable of neutralising or modulating production of anti-myelin
 PT basic protein

PS Disclosure: Page 15; 75pp; English.
 CC The present sequence represents a myelin basic protein (MBP) protein fragment used to produce MBP peptides. MBP peptides are capable of neutralising or modulating the production of anti-myelin basic protein.
 CC The present invention also describes a method for treating multiple sclerosis (MS). The method comprises administering to the patient an MBP peptide of the formula: R1-val-His-Phe-Asn-Ile-R2 where R1, R2 = H, OH or an amino acid residue and a polypeptide residue, provided that R1 and R2 are not both H or OH at the same time.
 SQ Sequence 46 AA;

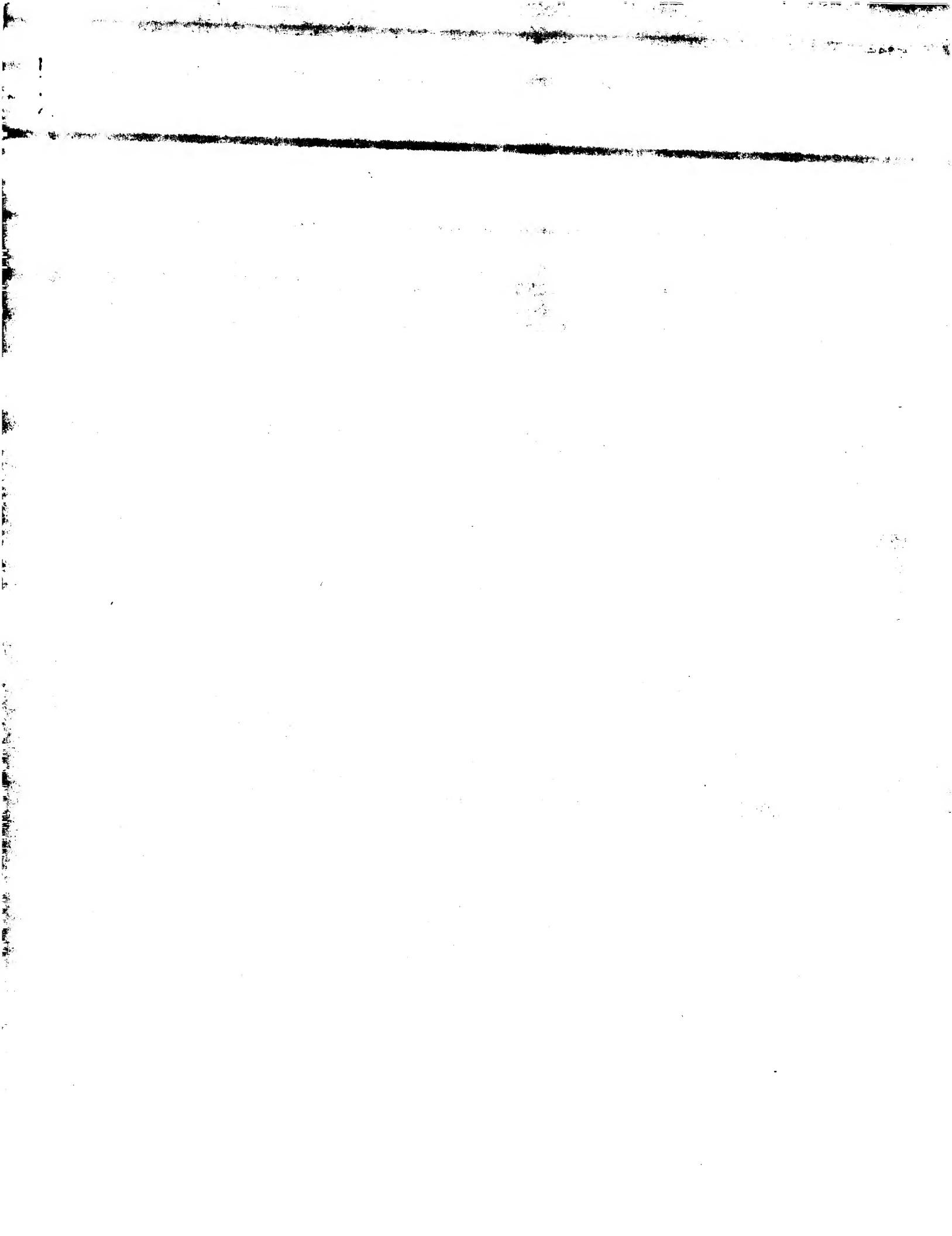
| Query Match | Score | DB 1; | Length | 46; |
|-----------------------|-------|--------------|----------|------------|
| Best Local Similarity | 26.9% | Pred. No. | 2.2e-38; | |
| Matches | 46; | Conservative | 0; | Mismatches |
| Indels | 0; | Gaps | 0; | |

Qy 62 RHPARTAHYSSLQPKSHGRDQDENENVHFRKNTVPRTPPSQKG 107
 Db 1 RHPARTAHYSSLQPKSHGRDQDENENVHFRKNTVPRTPPSQKG 46

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 Job time: 584 sec

Wed Sep 27 09:09:31 2000

us-09-218-277-12.rag



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DM of: US-09-218-277-12 to: GenEmbl: * out_format : pfs
Date: Sep 26, 2000 8:02 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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-LIST=45 -DCALIGN=200 -THR_SCORE=-0.5 -THR_MAX=100 -THR_MIN=0
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seq_documentation_block:
LOCUS HUMANMBP 1781 bp DNA PRI 08-MAR-1994
DEFINITION Human Goll-MBP gene, complete cds.
ACCESSION L18866
VERSION .1
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Homo sapiens; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1781)
REFERENCE Pribyl,T.M., Campagnoni,C.W., Kampf,K., Kashima,T., Handley,Y.W.,
AUTHORS McMahon,J. and Campagnoni,A.T.
TITLE The human myelin basic protein gene is included within a
179-kilobase transcription unit: expression in the immune and
central nervous systems
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (22), 10695-10699 (1993)
MEDLINE 94068468
FEATURES Location/Qualifiers
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    /cell_type="oligodendrogloma (ROG) cell line"
    /tissue_type="brain"
    /map="18q22-qter"
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 BASE COUNT 427 a 545 c 492 g 317 t
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 17 arnAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisa 34
 651 CACGAACTACATGGACCATGGAGATGGCTTCCTCCAGGCCACA 700
 34 rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
 701 GAGCACGGGCATCCtGACTCCATGGCGCAGTCCTTGCGTGACAGG 750
 51 GlyAlaProLysArgGlySerGlyIleAspSerIleAsp 67
 751 GGTCGCCAAAGGGGGCTGGCAAGGACTCACACCACGGCAAGAC 800
 67 ralaHistGlySerLeuProGlnLyserHisGlyArgGlySerGlnAspG 84
 801 TGGTCACTATGGCTCCAGCCAGAACTCACCGGGGACCCAAAGTG 850
 84 IuasnProValHisPhePheLysAsnIleValThrProArgThrPro 100
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 101 ProProSerGlnGlySerGlyIleLeuSerIleSerArgPheSerTr 117
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 117 pglyAlaGluGlyGlnArgProGlyPheGlyTyrglyArgSerAlaSerA 134
 951 GGGGCCGAAGGCCAGAGCCAGGATTTGGCTGAGGCGGCTGGCG 1000
 134 sptrLysserAlaHisLysGlyPheLysGlyValAlaGlnGlyThr 150
 1001 ACTATAATCGCTTCACAGGGATTCAGGGATCTGATGCCGGCAGC 1050
 151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerIleSerPr 167
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seq_documentation_block:
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 DEFINITION Human myelin basic protein (MBP) mRNA, complete cds.
 ACCESSION M13577.1 GI:187408
 VERSION M13577.1
 KEYWORDS myelin basic protein.
 SOURCE Human brain, mRNA to cDNA, clones pMBP-1 and pMBP-2.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 2139)
 AUTHORS Kamholz, J., de Ferra, F., Puckett, C. and Lazzarini, R.
 TITLE Identification of three forms of human myelin basic protein by cDNA cloning
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83 (13), 4962-4966 (1986)
 MEDLINE 86255714
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 CDS 37 . 552
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BASE COUNT 519 a 619 c 556 g 445 t
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 37 ATGGCGTCAGAAGAGACCCCTCCAGGCCGGATCAAGTACCTGGC 86
 17 arnAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisa 34
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 87 CACGAACTACATGGACCATGGAGATGGCTTCCTCCAGGCCACA 136
 34 rgAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
 137 GAGACACGGCATCTGACATCCATCGGCGTCTTGTGGCGTGCAGGG 186
 51 GlyAlaProLysArgGlySerGlyIleAspSerIleSerArgPheSerTr 67
 187 GTGGCGCAACGGGCTCTGGCAAGGACTCACCCGGCAAGAAC 236
 67 ralaHistGlySerLeuProGlnLysserHisGlyArgThrGlnAspG 84
 237 TGCTCAATGGCTCCCTGCCAGAAGTCAACGGGGACCCAAAGATG 286
 84 luAsnProValHisPhePheLysAsnIleValThrProArgThrPro 100
 287 AAACCCCGTAGCTCCACTTCATCAAGACATGTGAGCCTCGACACCA 336
 101 ProProSerGlnGlyLysGlyArgGlyLeuSerArgPheSerTr 117
 337 CCCCGTGCAGGAAARGGGAGAGSACTGTCCTCTAGCAGATTAAGCTG 386
 117 pglyAlaGluGlyGlnArgProGlyPheGlyTyrglyGlyArgAlaSerA 134

387 GGGGCCGAGGCCAGACCGGATTGGCTACGGAGGGTCCG 436
 134 SPTYRLSSerAlaHsLysGlyPhyLeuGlyValAspAlaGlyLysThr 150
 437 ACTATAATGGCTACAAGGATCAAGGAGTGATGCCAGGCACG 486
 151 LeuSerLysIlePhyLeuLeuGlyLysGlyAspSerArgSerGlySerPr 167
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 167 metAlaArgArg 171
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seq_name: qb_pr3:HUM215MBP

seq_documentation.block:

LOCUS HUM215MBP 622 bp DNA PRI 20-JAN-1996
 DEFINITION Homo sapiens synthetic myelin basic protein 21.5 kDa isoform gene,
 complete cds.

ACCESSION L41657.1

VERSION GT:1162921

KEYWORDS myelin basic protein; synthetic DNA; synthetic gene.

SOURCE Homo sapiens DNA.

ORGANISM Homo sapiens

REFERENCE 1 (sites)
 Kamholz,J., de Ferria,F., Puckett,C. and Lazzarini,R.
 Identification of three forms of human myelin basic protein by cDNA cloning
 Proc. Natl. Acad. Sci. U.S.A. 83 (13), 4962-4966 (1986)

REFERENCE 2 (bases 1 to 622)
 Nye,S.H., Pelfrey,C.M., Burkhardt,J.J., Voskuhl,R.R., Lenardo,M.J.
 and Mueller,J.P.

AUTHORS and Mueller,J.P.

TITLE Purification of immunologically active recombinant 21.5 kDa isoform of human myelin basic protein

JOURNAL Mol. Immunol. 32 (14-15), 1131-1141 (1995)

MEDLINE 96128281

COMMENT Sequence M13577 overlaps this sequence.

FEATURES Location/Qualifiers

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 1 MetAlaSerGlnLysArgProSerGlnArgHisCysLeuLysTyrLeuAl 17
 4 ATGcGTcAGAAACGTCAGTCAGCTCAGGCTCAAATACCTGGC 53
 17 athAlaSerThrMetAspHisAlaArgHisGlyPhetLeuProGlyAs 34
 54 CACGCCACACCATGGACCATGGCCATCTGGCTTCCTGGCGTCAC 103
 34 rGAsPThrGlyLileLeuAspSerIleGlyArgPhpheGlyGlyAspArg 50
 104 GTGACACCGCAGCTCTGGCTCATGGCTGAAAGGCCGTGGCTTCGGTGA 153
 51 GlyAlaProLySArgGlySerGly..... 58
 154 GGtGGCCAAACGTCAGCTGGCTCTGGAAAGGCCGTGGCTTCGGTGA 203
 58 58
 204 TAGGCCGCTGCCGCTCATGCCGTAGCCAGGCCGGCTGTGCCAACATC 253
 59 .LysAspSerHisProAlaArgAlaHistYrySerLeuPro 74
 254 ACARAGACTCCACACCCGGCAGTACCGGCACTATGCTCCCTGCGC 303
 75 GlnLysSerHisGlyArgGlnAspGluAsnProValHisPhePhe 91
 304 CAGAAATCCACGCGCTACCCAGATGAAAACCGGTGTCACATCT 353
 91 ElsAsnIleValThrPraMgTrProProSerGlnGlyLysGly 108
 354 CAAAAACATGTGACCCCCCGTAGCCCTTCTCGCTGGCAAAGGCC 403
 108 rggLYLeuSerLeuSerArgPheserTrgLyAlaGluGlyGlnArgPro 124
 404 GTGGCCCTGCCCTAGCCCTTCTCGCTGGCCACCGTC 453
 125 GlyPheGlyTyrglyGlyArgAlaSerAspTrpTlySerAlaHisLysGly 141
 454 GGCTTCGGTAGCGGGCTGCTCCGACTATAATCGCTCACAAAGG 503
 141 YPheLysGlyValAspAlaPheGlnGlyThrLeuSerLysIlePheLysLeuG 158
 504 CTTCAAAGGGTGTGATGCCAGGGCACCTGTCCAAATTTCAACCTG 553
 158 LysGlyArgAspSerArgSerProMetAlaArgArg 171
 554 GCGGCCGTTATAAGCGTTCTGGCTCCAGTGGCTAGCT 594

seq_name: qb_pr2:HUMMBPC

seq_documentation.block:

LOCUS HUMMBPC 1261 bp mRNA 07-JAN-1995
 DEFINITION Human 21.5 kD myelin basic protein (RK41) mRNA, complete cds.

ACCESSION M30515
 VERSION M30515.1 GI:187412

KEYWORDS alternative splicing; myelin basic protein.

SOURCE Human spinal cord, cDNA to mRNA.

ORGANISM Homo sapiens
 Eukaryota; Primates; Chordata; Craniata; Vertebrata; Mammalia;
 1 (bases 1 to 1261)
 REFERENCE Roth,H.J., Kronquist,K.E., Kerlero de Rosbo,N., Crandall,B.F. and
 Campagnoni,A.T.

TITLE Evidence for the expression of four myelin basic protein variants
 in the developing human spinal cord through cDNA cloning
 J. Neurosci. Res. 17 (4), 321-328 (1987)

JOURNAL 8731171
 MEDLINE 8731171
 FEATURES Location/Qualifiers
 Source 1..1261

| | | alignment_scores | Quality: | 836.00 | Length: | 172 |
|--------------------------|--|-------------------|----------|--------|-------------|-----|
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| 233 | TGCTCACTACGGCTCCGTGCCCGAGCTCACACGCCGACCCAAAGATG | 282 | | | | |
| 84 | IuasnProvalylHsPhePhelyAsnIleLevalthriProArgThrPro | 100 | | | | |
| 283 | AAARCCCCGTAGTCCACTCTAACANCATGTACGCCGACACCA | 332 | | | | |
| 101 | ProProserGlyGlyArgGlyLeuSerIleSerArgPheSerI | 117 | | | | |
| 333 | CCCCGTCGAGGAAG..... | 350 | | | | |
| 117 | PglyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA | 134 | | | | |
| 351 | GGGGCCGAAGGCCAGAGACAGGATTGGCTACCGAGGAGGGTCGG | 399 | | | | |
| 134 | SPTYRlysSerAlaIhtLysGlyPhyLysGlyValAspAlaGlnGlyThr | 150 | | | | |
| 400 | ACTTAAATTCGCTCTCACAGGGTTCTCAGGGAGTCATGCCAGGGCAAG | 449 | | | | |
| 151 | LeuSerIlysIlePhyLysLeuglyGlyArgAspSerArgSerGlySerPr | 167 | | | | |
| 450 | CTTTCACAAATTCTTANGCTGGAGAAAGATACTGCCTGGATCACCC | 499 | | | | |
| 167 | OmetAlaArgArg | 171 | | | | |
| 500 | CATGGCTAGAACCC | 512 | | | | |
| seq_name: | gb_ro.RNO132897 | | | | | |
| seq_documentation_block: | | | | | | |
| LOCUS | RNO132897 | 510 bp | mRNA | ROD | 11-FEB-1999 | |
| DEFINITION | Rattus norvegicus mRNA for myelin basic protein, | 18.5 kDa isoform. | | | | |
| ACCESSION | AJ132897 | | | | | |
| VERSION | AJ132897.1 | | | | | |
| GI: | 4454314 | | | | | |
| KEYWORDS | mbp gene; myelin basic protein. | | | | | |
| NORMRAT | Rattus norvegicus | | | | | |
| EUKARYOT | Metazoa; Chordata; Craniata; Vertebrata; Mammalia; | | | | | |
| EUTHERIA | Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | | | | |
| 1 | (bases 1 to 510) | | | | | |
| REFERENCE | Lobell, A. M. | | | | | |
| AUTHORS | Direct Submission | | | | | |
| TITLE | Submitted (09 FEB-1999) Lobell A.M., Karolinska Institute, Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm, SWEDEN | | | | | |
| REFERENCE | 2 (bases 1 to 510) | | | | | |
| AUTHORS | Lobell, A. M. and Wigzell, H. | | | | | |
| JOURNAL | Unpublished | | | | | |
| FEATURES | Location/Qualifiers | | | | | |
| source | 1..510 | | | | | |
| | /organism="Rattus norvegicus" | | | | | |
| | /strain="Lewis rat" | | | | | |
| | /db_xref="taxon:10116" | | | | | |
| gene | 1..510 | | | | | |
| CDS | /gene="mbp" | | | | | |
| | /gene="mbp" | | | | | |
| | /note="18.5 kDa isoform" | | | | | |
| | /codon_start=1 | | | | | |
| | /product="myelin basic protein" | | | | | |
| | /protein_id="CAA10806_1" | | | | | |
| | /db_xref="GI:4454315" | | | | | |
| | /translation="WASQCRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGFESGDGAPRKSGKDHSRTRTHGSLPKSQSRQDENVVHFKN1VTPRPPPSKSGRKGRLLSPEFWGADQKPGFYGRASDYSKSAHKFGAYDAQGTLISKIFKGGRRSGPARR" | | | | | |
| BASE COUNT | 134 a | 155 c | 139 g | 82 t | | |
| ORIGIN | | | | | | |

TITLE Identification of a cDNA coding for a fifth form of myelin basic protein in mouse
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84 (3), 886-890 (1987)
 MEDLINE 87118269
 COMMENT Draft entry and computer-readable sequence for [1] kindly provided by A.R.Campagnoni, 30-MAR-1987.
 As many as eight myelin basic proteins can be encoded by the same gene by alternative splicing. The sequence below is missing exons 2 and 5 of the gene and encodes a 17.22 kDa myelin basic protein. The variations in the 3' untranslated regions between the two clones may be reverse transcriptase errors [1].

FEATURES

source

1. 1935
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /sub_species="domesticus"
 /db_xref="taxon:10090"
 /clone="NK-W18."
 /dev_stage="18-day-old"
 /tissue_type="brain"
 <!. .452
 /note="myelin basic protein"
 /codon_start=3
 /protein_id="AAB59712.1"
 /db_xref="GI:199051"
 /translation="RSKYLATASTMDHARHGFLPRHDTGILDSIGREFGSDRGAPKR GSQKDSRTHYSLFQKSQHGRDODENPVHFENIVTRTPPSQGRGAEGKPGP FGGRGASDYKSAHKGFKAQDAQGLSKIFLGGDRSRSQSPMARR"
 variation 1023
 /note="t in M78; c in M72"
 /replace="c"
 variation 1700
 /note="t in M78; c in M72"
 /replace="c"
 variation 447 a
 545 C 517 9 428 t 2 others
 BASE COUNT 35 bp upstream of Avall site.

ORIGIN

align seg 1/1 to: MUSMBP78M from: 1 to: 1939
 Quality: 716.50 Length: 161
 Ratio: 4.908 Gaps: 4
 Percent Similarity: 90.683 Percent Identity: 87.578

alignment_block: US-09-218-277-12 x MUSMBP78M

align seg 1/1 to: MUSMBP78M from: 1 to: 1939
 Quality: 716.50 Length: 161
 Ratio: 4.908 Gaps: 4
 Percent Similarity: 90.683 Percent Identity: 87.578

alignment_scores:

13 SerIleSerLeuAlaThrAlaSerThrMetAspHisAlaArgHisGlyph 29
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 6 TCCAGTACTGCCACAGCACTGACATTGGCATGGGATGGTT 55
 29 eLeuProArgHisArgAspThrGlyIleLeuAspSerIleGlyArgPheP 46
 56 CCTCCAAAGCACAGAGAACGGCATCTGGGCATCTGGGCTCT 105
 46 heGlyGlyAsparGlyAlaProIysArgGlySerGlySerGlyAspSerHis 62
 106 TTGGGTGACAGGGTGCGCCCAAGCGGGCTGGCATGGACTCACAC 15.5
 63 HisProAlaArgThrAlaHistGlySerLeuProGlnLysser...Hi 78
 156 ... ACCGAACTACCAATTGGCCCTGCCCAAGGGCACA 199
 78 sGlyArgArgGluAsnProValIysIlePhePheLysAsnIleV 95
 200 CGCGGACCAAGATGAAACCAGTACCTTCATAAACATG 249
 95 alThrProArgThProProSerGlyIysGlyArgGlyLeuSer 111
 250 TGACACCTCGAACACCACCTCCATCCAAAGGGARG..... 284
 112 LeuSerArgPheSerTrpGlyAlaIgluGlyGlyGlyArgProGlyPheGlyTy 128

align seg 1/1 to: RATMBP2A from: 1 to: 612
 Quality: 615.50 Length: 171
 Ratio: 4.809 Gaps: 3
 Percent Similarity: 74.854 Percent Identity: 72.515

alignment_block: US-09-218-277-12 x RATMBP2A

align seg 1/1 to: RATMBP2A from: 1 to: 612
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 41 ATGGCATCACAGAAAGACCTCACAGCGTCAAGTACTGTC 90
 17 aThrAlaSerThrMetAspHisAlaArgHisGlySerGlyAspSerIle 34
 91 CACAGCAAGTACATGACATGGCCATGGCTCTCCAAAGCACA 140
 34 rGlyAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
 141 GAGACACGGCTCTGATCCATCGGCGTCTTAAGCTGACAGG 190
 51 GlyAlaPzLysArgGlySerClyLysAspSerHisHisProAlaArgTh 67

JOURNAL Cell 34, 799-806 (1983)
 MEDLINE 84066484
 COMMENT mbp's have been found in rats, small (m-r=14,000) and large (m-r=18,500). The sequence shown is for the small mbo, however the

51 GlyAlaProLysArgGlySerGlyLysAspSerSerHisProAlaArgThr 67
 150 CACGTRCCCCGGGGCTTGCAAGGATA...CACCGAGGGC 196
 67 RalaHistTyrySerLeuProGlnLysSer...HisGlyArgThrGlnA 83
 197 CAGCCATGTAGCTTACATCCCCAGGGTCAGCATGGCGGCCGGTG 246
 83 SPGLuAsnProValValHisPhePheLysAsnIleValThrProArgThr 99
 247 AGCACAAACCTCTGTTAGCTTACACTTCTAACAGAACATGTCCTACCCGTACT 296
 100 ProProProSerGlnGlyLysGlyLeuSerLeuSerArgPheSe 116
 297 CCTCCCTCAAATGCAAGGAAGGAGGACTGCCCCTACAGATTAG 346
 116 RTRPGLYAlaGluGlyGlnArgProGlyPheGlyLysGlyArgAlaS 133
 347 CTGGGTGGTAAGGCAACAGCCGGATAAGGA...AGTGGAAATTCT 393
 133 EraspTyryLysSerAlaHistGlyPheLysGlyVal....AspAla 147
 394 ATGAGGACAAATCTGTCACAAGGGACACAAGGGATCCTATCACAGGGC 443
 148 GlngGlyThrLeuSerLysIlePheLysLeuGlyGlyArg..... 160
 444 CAGGGACTCTTCCAAATCTTAACTGAGGAGCTCTGGCTCCGGCC 493
 161 .AspSerArgSerGlySerProMetAlaArgArg 171
 494 TGGATGGGTTGGCTTACAGATGGCAGGGC 527

seq_name: gb_to:RN0132896
 seq_documentation_block:
 LOCUS RN0132896 465 bp mRNA ROD 11-FEB-1999
 DEFINITION Rattus norvegicus mRNA for myelin basic protein, 17 kDa isoform.
 ACCESSION AJ132896
 VERSION AJ132896.1 GI:4454312
 ISOTFORM; mbp gene; myelin; myelin basic protein.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1. (bases 1 to 465)
 AUTHORS Lobell,A.M.
 TITLE Direct Submission
 JOURNAL Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute,
 Microbiology and TumorbioLOGY center, Box 280, 171 77 Stockholm,
 SWEDEN
 FEATURES /organism="Rattus norvegicus"
 /strain="Lewis rat"
 /db_xref="taxon:10116"
 gene
 /gene="mbp"
 CDS
 /gene="mbp"
 /note="17 kDa isoform"
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 /db_xref="GI:4454313"
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 RTQDENPVVHFVKIVTPTPPPQQGKGRGLSLSRSMNGGRDSSGSPSIARR"

BASE COUNT
 ORIGIN 117 a 153 c 120 g 75 t

OM of: US-09-218-277-12 to: N_Geneseq_36:* out_format : pfs
 Date: Sep 26, 2000 8:19 PM
 About: Results were produced by the Gencore software, version 4.5.
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPXT=0.050 XGAPOP=10.000 XGAPXT=0.500
 -DELOP=6.000 -DFELEX=7.000 -SPART=1 -MATRIX=blossum62
 -TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
 -NORM_ext -MINDEN=0 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
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Search information block:
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 Query length: 171
 Database: N_Geneseq_36:
 Sequences: 311585
 Database length: 12596042
 Search time (sec): 55.050000

score_list:

| Sequence | Strd | Orig | ZScore | Escore | Len | Documentation |
|----------------------|------|--------|---------|----------|--------|--|
| N_Geneseq_36:T30269 | + | 922.00 | 1389.40 | 8.6e-70 | 516 | Human myelin basic protein cod1 |
| N_Geneseq_36:T35561 | + | 922.00 | 1389.40 | 8.6e-70 | 516 | Human myelin basic protein (MBP) |
| N_Geneseq_36:T41889 | + | 899.00 | 1353.54 | 8.6e-68 | 594 | Human myelin basic protein (foetal myelin basic protein MBP) |
| N_Geneseq_36:T41896 | + | 899.00 | 1353.28 | 8.9e-68 | 612 | Foetal myelin basic protein MBP |
| N_Geneseq_36:T41897 | + | 899.00 | 1353.28 | 8.9e-68 | 612 | Foetal myelin basic protein MBP |
| N_Geneseq_36:T41893 | + | 899.00 | 1348.08 | 1.7e-67 | 1122 | 1 MBP4 chimera (MBP21.5-delta PLF MP3 chimera (MBP21.5-delta PLF |
| N_Geneseq_36:T41892 | + | 899.00 | 1347.84 | 1.8e-67 | 1155 | MP4-PE chimera (MBP21.5-delta PLF MP3-PE chimera (MBP21.5-delta PLF) |
| N_Geneseq_36:T41895 | + | 899.00 | 1345.03 | 3.3e-67 | 1146 | MPN4P4 chimera (MBP21.5-delta PLF-PE chimera (delta PLP4-PEBP21. |
| N_Geneseq_36:T41894 | + | 894.00 | 1340.53 | 4.6e-67 | 1125 | MPN4 chimera (delta PLP4-PEBP21. |
| N_Geneseq_36:Q49976 | + | 160.00 | 234.17 | 1.9e-05 | 1164 | Nucleotides 301-1464 of rat my |
| N_Geneseq_36:Q48975 | - | 135.00 | 196.63 | 0.0024 | 1147 | 1 Encodes RB35 protein from rat |
| N_Geneseq_36:T47123 | + | 134.00 | 200.38 | 0.0015 | 621 | 1 cDNA encoding soluble fused MHC |
| N_Geneseq_36:T47110 | + | 107.00 | 179.32 | 0.0218 | 63 | 1 Human BPP-PE chimeric protein co |
| N_Geneseq_36:T47117 | + | 107.00 | 179.32 | 0.0218 | 63 | 1 Human BPP-PE chimeric protein co |
| N_Geneseq_36:T67168 | + | 107.00 | 179.32 | 0.0218 | 63 | 1 BPP-PE chimeric protein synthesis |
| N_Geneseq_36:V62133 | + | 103.00 | 127.79 | 1.6e-20 | 12700 | 1 HSV-2 strain SB5 Contig ID 10 |
| N_Geneseq_36:T67172 | + | 102.00 | 171.38 | 0.0604 | 66 | 1 Human BPP-PE chimeric protein co |
| N_Geneseq_36:T67169 | + | 102.00 | 171.38 | 0.0604 | 66 | 1 Human BPP-PE chimeric protein co |
| N_Geneseq_36:V62160 | + | 102.00 | 126.98 | 1.7e-97 | 11705 | 1 HSV-2 strain SB5 Contig ID 16 |
| N_Geneseq_36:T62276 | + | 101.00 | 107.22 | 1.26e-43 | 117213 | 1 HSV-2 strain SB5 Contig ID 1 |
| N_Geneseq_36:T60704 | + | 101.00 | 149.60 | 0.9870 | 702 | 1 cDNA encoding soluble fused MHC |
| N_Geneseq_36:V05110 | - | 93.50 | 106.10 | 261.49 | 30001 | 1 Maize Bxi cDNA (DIMBOA biosyn |
| N_Geneseq_36:V5273 | - | 94.50 | 134.76 | 6.62 | 1508 | 1 Human enzyme-related antisense |
| N_Geneseq_36:X53491 | - | 94.50 | 96.09 | 622.22 | 612 | 1 Human adenosine A1 receptor |
| N_Geneseq_36:X23299 | + | 93.50 | 124.15 | 25.83 | 3656 | 1 Human SPA-1 cDNA. New human SP |
| N_Geneseq_36:V622781 | + | 93.50 | 122.51 | 31.86 | 4425 | 1 Human interlein-1 receptor |
| N_Geneseq_36:T61016 | - | 92.00 | 106.10 | 261.49 | 30001 | 1 Total DNA sequence from cosmid |
| N_Geneseq_36:X05110 | - | 93.50 | 106.10 | 261.49 | 30001 | 1 S. aureofaciens DNA in cosmid |
| N_Geneseq_36:V62249 | + | 93.00 | 120.86 | 40.42 | 5032 | 1 HSV-2 strain SB5 Contig ID 95 |
| N_Geneseq_36:Y10362 | - | 92.00 | 120.58 | 40.80 | 4257 | 1 Infected cell protein number 4 |
| N_Geneseq_36:V68520 | - | 92.00 | 120.58 | 40.80 | 4257 | 1 The nucleotide sequence of the |
| N_Geneseq_36:T85473 | - | 92.00 | 116.56 | 68.33 | 6803 | 1 Human HNET sequence from P1 |
| N_Geneseq_36:V16305 | - | 92.00 | 116.56 | 68.33 | 6803 | 1 Genomic DNA encoding human net |
| N_Geneseq_36:Q76113 | + | 92.00 | 111.70 | 127.56 | 12001 | 1 HSV-L/SR region. Herpes Simp |
| N_Geneseq_36:V29446 | + | 91.00 | 130.58 | 11.32 | 1113 | 1 Calcium ion channel alpha1 sub |
| N_Geneseq_36:V43617 | - | 91.00 | 126.89 | 18.16 | 1711 | 1 Human secreted protein 17 enco |
| N_Geneseq_36:T38809 | - | 91.00 | 124.04 | 26.19 | 2386 | 1 Marmoset intracellular vitamin |
| N_Geneseq_36:V29472 | + | 91.00 | 115.07 | 70.72 | 6789 | 1 Calcium ion channel alpha1 sub |
| N_Geneseq_36:Q84660 | + | 91.00 | 113.89 | 96.22 | 7791 | 1 Human neuronal calcium channel |
| N_Geneseq_36:Q84659 | + | 91.00 | 113.88 | 96.46 | 7808 | 1 Human neuronal calcium channel] |

seq_name: N_Geneseq_36:T30269
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 ID T30269 standard; DNA: 516 BP.
 AC 09-Nov-1996 (first entry)
 PA (NEUR-) NEUROKINE BIOSCIENCES INC.
 STRD) UNIV STANFORD MEDICAL CENT.
 PI Conlon PJ, Gaul A, Ling N, Steinman L;
 DR WP1; 96-288534-77/
 PT Peptide analogue of human myelin basic protein - has Lysine 91
 PR replaced by another amino acid, useful to treat multiple sclerosis
 PS Disclosure: Figure 1: 30OP; English.
 CC A peptide analogue comprising amino acids 87-99 of human myelin
 CC basic protein (MBP), where Lys91 is substituted for another amino
 CC acid can be used to treat and prevent multiple sclerosis. The
 CC peptide analogue is administered at a dosage range of 5-50 mg/kg.
 SQ Sequence 516 BP; 130 A; 153 C; 149 G; 84 T;
 alignment_scores:
 US-09-218-277-12 x T30269 ..
 US-09-218-277-12 x T30269 from: 1 to: 516
 Align seg 1/1 to: T30269 from: 1 to: 516
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 1 ATGGCTCACAGAAGACCCCTCCAGAGGACGATTCAGTACTGC 50
 17 aThrAlaserThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
 51 CACAGCAGTACCATGACCATTGCCAAAGCACA 100
 34 rgasphrGlyLileLeuaspSerIleGlyArgphepheGlyAspArg 50
 1 ATGGCTCACAGAAGACCCCTCCAGAGGACGATTCAGTACTGC 50
 101 GAGACAGGGGATCCTTGACTCCATGGCTTCAGGGTACAGG 150
 51 GLYAlaProlysArgLYSerGlyLysSerGlySerLysProAlaArgH 67
 151 GTGGCCAAAGGGGGCTCAGGAGCTCACACCCGGCAAGATG 200
 67 rAlaHistrglySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
 201 TGCTCACTATGCTCCCTGCCAGAGTCAACGCCGGACCCAAAGATG 250
 84 LuAsnProvalylHisPheIleLysAsnIlevalThrProArgThrPro 100
 251 AAAACCCGTAGTCACITCTCAAGAACATTGACGCCCTGCACACA 300

101 ProProSerGlnGlyLysGlyArgGlyLeuSerIleSerArgPheSerTr 117
 301 CCCCCGGTCAGGGAAAGGGAGGACTCTGAGGATTTAGCTG 350

117 PGlyAlaGluGlyGlnArgProGlyPheClyTgGlyArgTgAlaSerA 134
 351 GGGGGCCGAGGCCAGAGCCAGGATTGGCTACGGGSCAGGGCTCG 400

134 SPtRLysSerAlaHisLysGlyAlaAspAlaGlnGlyThr 150
 401 ACTATAAACGGCTCACAGGGATTCAAGGGATCAGGGATCAGGCCGGACG 450

151 LeuSerLysIlePheLysIleGlyGlyArgAspSerArgSerGlySerPr 167
 451 CTTTCAAAATTGTTAACGTGGGAGGAAGATAAGTCGCTCTGATCAC 500

167 OMAlaAlaArg Arg 171
 501 CATGGCTAGACGC 513

seq_name: N_Genesed_36_T32561

seq_documentation_block:

ID T32561 standard; DNA; 516 BP.

AC T32561;

DT 07 NOV-1996 (first entry)

DE Human myelin basic protein (MBP) coding sequence.

KW Myelin basic protein; MBP; multiple sclerosis; MS; competition; inhibition; major histocompatibility complex; MHC; thymocyte; T cell; experimental allergic encephalomyelitis; EAE; analogue; treatment; prevention; ss.

KW Homo sapiens.

OS

FR Key

FT 1 . 516

FT /*tg-^a

FT /product= Myelin basic protein .

PN W09616066-A1.

PD 30 MAY-1996.

PR 16-NOV-1995; U14403.

PA (NFDR-) NEUROCRINE BIOSCIENCES INC.

PI Conlon PJ, Gaur A, Ling N, Steinman L;

DR WPI: 96-26852/27.

DR P-PSDB: R99580.

PR peptide analogues of human myelin basic protein - useful for treatment of multiple sclerosis

PS Disclosure: Figure 1: 61pp; English.

CC peptide analogues comprising at least seven amino acids from residues 86-99 of human myelin basic protein (MBP), can be used to treat multiple sclerosis by competing for the binding of native MBP peptide to MHC and by not causing proliferation of an MBP reactive T-cell line. The peptide analogues also inhibit the induction of experimental allergic encephalomyelitis (EAE) by MBP in rodents.

CC The peptide analogues have a reduced susceptibility to proteolysis in vivo.

SQ Sequence 516 BP; 130 A; 153 C; 149 G; 84 T;

alignment_scores:

Quality: 922.00 Length: 171

Ratio: 5.392 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-218-277-12 x T32561 ..

Align seq 1/1 to: T32561 from: 1 to: 516

1 MethAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17

1 ATGGCTTCAGGAGACCTCCAGGGATCCAAGTACCTGGC 50

17 arnAlaSerThrNetAspHisAlaArgHisGlyPheLeuProArgHisa 34

CC T41896-97). Recombinant MBP 21.5 polypeptides are useful in the
CC clinical assessment, diagnosis and treatment of MS.
SQ Sequence 594 BP; 143 A; 184 C; 171 G; 96 T;

alignment_scores:
 Quality: 899.00 Length: 197
 Ratio: 5.257 Gaps: 1
 Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:
 AY09-218-277-12 x T41899 ..

Align seq 1/1 to: T41899 from: 1 to: 594

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
 1 ATGGCCTCACAGAAAGACCTCCAGAGGCCAGGATCCAGTACCTGGC 50
 17 alnAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
 51 CACAGAAAGTACATGGACCATGGCAGGCATGCTTCCTCAAGCACA 100
 34 rGaspThrGlyLileLeuAspSerIleGlyArgPhePheGlyAspArg 50
 101 GAGACAGGGCATCCITGACTCATGGCCCTTCITTGCGGTGACAGG 150

51 GlyAlaProLysArgGlySerGly..... 58
 151 GTGTGCCCCAARGGGGGCTCTGCAAGGTACCCCTGGCTAAAGCGGGCCG 200

58 58

201 GAGCCCTCTGCCTCTGCGCTCTGCGACGCCAACCTGGCTGTGCAACATGT 250

59 .. LysAspSerHisHisProAlaArgThrAlaHistyryGlySerLeuPro 74
 251 ACAAGGACTCACACCAACCCGGGACCCAAAGTGTCACTATGGCTCCCTGCC 300

75 GlnLysserHisGlyArgThrGlnAspGluAsnProValAlaHisPhePh 91
 301 CAGAAAGTCACAGGGGGACCCAAAGTGAAGAACCCGGTAGTCACATTCTT 350

91 eLysAsnIleValThrProArgThrProProserGlnLysGlyA 108
 351 CAGAACATTTGACCCCTGACACACCCCCGIGCAGGGAAAGGG 400

108 rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
 401 GAGGACTGTCCCTGAGGAGATTAGCTGGGGGCCAAGGCCAGACCA 450

125 GlyPheGlyTyrcGlyGlyArgGalaSerAspTyrLysSerAlaHisLysG 141
 451 GGATTGGCTTGGAGGGCAGGGTCCGACTATAATGGCTCACAGGG 500

141 pHeLysGlyVyalAspAlaGlnGlyIhrLeuSerLysIleheLysLeuG 158
 501 ATTCAAGGGATGAGCCAGGAGCTTCATCCAAATTCAAGCTGG 550

158 LyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
 551 GAGGAAGAGATAAGTCGCTCTGATACCCTAGCTAGACGC 591

seq_name: N_Geneseq_36:T41896

seq_documentation_block:

ID T41896 standard; DNA; 612 BP.

AC T41896;

DT 01-FEB-1997 (first entry)

DE Foetal myelin basic protein MBP+X2Cys81/bact. DNA.

KW Myelin basic protein; MBP; MBP-X2Cys81; proteolipid protein; PLP;

KW multiple sclerosis; autoimmune disease; diagnosis; therapy;

KW T-lymphocyte; T-cell; aneity; apoptosis;

Synthetic.
 W0934622-A1.

OS PN W0934622-A1.

PD 07 NOV-1996; 005611.

PF 22-APR-1996.

PR 02-MAY-1995; US-431648.

PR 02-MAY-1995; US-431644.

PR 07-JUN-1995; US-482114.

PA (ALEX-) ALEXION PHARM INC.

(USSH) US DEPT. HEALTH & HUMAN SERVICES.

PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;

NYE SH, Peiffer CM, Squinto SP, Wilkins JA;

WPI: 96-205898/50.

DR P-PSDB; W06101.

DR P-PSDB; W06101.

New human myelin basic protein and proteolipid protein variant(s) - used in the assessment, diagnosis and treatment of multiple sclerosis

PT Disclosure: Page 81-82; 156pp; English.

PS CC A DNA sequence (T41896) codes for the human 21.5 kDa foetal isoform (W06107) of myelin basic protein, MBP-X2Cys81/bact., and utilises bacterially-preferred codons in place of the native human codons (see also T41899). This increases prod. of the MBP in E. Coli by at least 50%. Recombinant MBP 21.5 polypeptides (see also W00999 and W06108) are useful in the clinical assessment, diagnosis and treatment of MS.

Sequence 612 BP; 117 A; 215 C; 166 G; 114 T;

alignment_scores: Alignment seg 1/1 to: T41896 from: 1 to: 612

PS Quality: 899.00 Length: 197

PS Ratio: 5.257 Gaps: 1

PS Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block: alignment_block:
 US-09-218-277-12 x T41896 ..

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
 1 ATGGCCTCACAGAAAGACCTCCAGAGGCCAGGATCCAGTACCTGGC 50
 17 alnAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
 51 CACAGAAAGTACATGGACCATGGCAGGCATGCTTCCTCAAGCACA 100
 34 rGaspThrGlyLileLeuAspSerIleGlyArgPhePheGlyAspArg 50
 101 GAGACAGGGCATCCITGACTCATGGCCCTTCITTGCGGTGACAGG 150

51 GlyAlaProLysArgGlySerGly..... 58
 151 GTGTGCCCCAARGGGGGCTCTGCAAGGTACCCCTGGCTAAAGCGGGCCG 200

| | | |
|---|---|---|
| 125 GlypheGlyTyrglyArgLysAlaserAspTyrLysSerAlaHisLysG1 | 141 | 151 GGTGCCCGGAAACGTCGCTCTGGCAAGTGGCTGAAACGGCCG 200 |
| 451 GGCTTCGGTTAACGGGGCCCTGGCTCGACTATAATCTCACAAAGG 500 | 58 | 58 |
| 141 yPhelysGlyvalAspAlaGlnGlyThrLeuSerLysilePhelysLeug 158 | 158 | 59 . LysasparSerHisIleProAlaArthralaHistylGlySerLeuPro 74 |
| 501 CTCAAAGGGTGGATGCCAGGGTACCTGTCGAAATTCAACTGG 550 | 251 ACAAAACTCCACCCGGCTGACCGGCACATGGTCCCTGCCG 300 | 75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValYalHissphePh 91 |
| 158 lyGlyArgAspSerArgSerglySerProMetAlaArgArg 171 | 301 CAGAAATCCCACGGCGTACCCAGGTGAATGGCTAGCATGGTAGCCT 591 | 91 ElysAllevAlaThnProAgtgthrProptoproserGlyArgLysGly 108 |
| 551 GGGCGGTGATAGCGGTTCTGGCTCTGGATGGCTAGCATGGTAGCCT 591 | 351 CAAACACATGACCCGGCTACCCGGCCGCTGACTATAATCTGCTCACAAAGG 400 | 108 rgglyLeuSerLeuSerArgPheSerTrpGlyAlaGlyGlnArgPro 124 |
| eq_name : N_Geneseq_36:T41897 | 401 GTGGCTGTCCCTGACCGTTCAGGGGCCAAAGGCAAGCTCCG 450 | 125 GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisGly 141 |
| eq_documentation_block: | 451 GGCTTCGGTTACGGCGGCCGCGTCGACTATAATCTGCTCACAAAGG 500 | 141 IlyArgLysGlyAlaSerAlaGlyGlnGlyThrLeuSerLysileHelyLeuG 158 |
| D T41897 standard; DNA; 612 BP. | 501 CTTCAAGGGCTGGATGCCAGGGTACCTGTCGAAATTCAACTGG 550 | 158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171 |
| C T41897; | 551 GGGCGGTGATAGCGCCTCTGGCTCCGATGGCTAGCATGGTAGCCT 591 | 551 551 GGGCGGTGATAGCGCCTCTGGCTCCGATGGCTAGCATGGTAGCCT 591 |
| T 01-FEB-1997 (first entry) | seq_name: N_Geneseq_36:T41893 | seq_name: N_Geneseq_36:T41893 |
| Foetal myelin basic protein MBP+XSer81/bact. | seq_documentation_block: | seq_documentation_block: |
| E Myelin basic protein; MBP; MBP+XSer91; proteolipid protein; PLP; | ID T41893 standard; DNA; 1122 BP. | ID T41893 standard; DNA; 1122 BP. |
| W multiple sclerosis; autoimmune disease; diagnosis; therapy; | AC T41893; T41894; | AC T41893; T41894; |
| W T-lymphocyte; T-cell; anergy; apoptosis; ds. | DT 01-FEB-1997 (first entry) | DT 01-FEB-1997 (first entry) |
| S synthetic. | DE MPB Chimera (MPB21.5-delta PLP4 fusion) DNA. | DE MPB Chimera (MPB21.5-delta PLP4 fusion) DNA. |
| W W0934622-A1. | KW Proteolipid protein; PLP; delta PLP4; myelin basic protein; | KW Proteolipid protein; PLP; delta PLP4; myelin basic protein; |
| D 07-NOV-1996. | R 02-MAY-1995; US-431646. | R 02-MAY-1995; US-431646. |
| F 22-APR-1996; US05611. | R 02-MAY-1995; US-431644. | R 02-MAY-1995; US-431644. |
| F 02-MAY-1995; US-431644. | R 02-MAY-1995; US-431644. | R 02-MAY-1995; US-431644. |
| R (ALEX-) ALEXION PHARM INC. | R 07-JUN-1995; US-482114. | R 07-JUN-1995; US-482114. |
| A (USSH) US DEPT HEALTH & HUMAN SERVICES. | R 07-JUN-1995; US-482114. | R 07-JUN-1995; US-482114. |
| L Lenardo MJ, Natis L, McFarland HF, Mueller EE, Mueller JP; | R WPI: 96-505898/50. | R WPI: 96-505898/50. |
| I Nye SH, Pelfrey CM, Squinto SP, Wilkins JA; | R P-PSDB; W06108. | R P-PSDB; W06108. |
| R New human myelin basic protein and proteolipid protein variant(s) - used in the assessment, diagnosis and treatment of multiple sclerosis | Q Sequence 612 BP; 117 A; 215 C; 166 G; 114 T; | Q Sequence 612 BP; 117 A; 215 C; 166 G; 114 T; |
| T Disclosure: Page 82-83; 156pp; English. | P Alignment scores: | P Alignment scores: |
| C A DNA sequence (T41897) codes for the human 21.5 kDa foetal isoform (W06108) of myelin basic protein, MBP-x2Ser1, and utilises codons that are preferentially used in highly-expressed bacterial genes and includes a sequence coding for an N-terminal hexahistidine tag. This facilitates large-scale Prodn. and purification of MBP 21.5 polypeptide in bacterial host cells. Recombinant MBP 21.5 polypeptides (see also W00399 and W06107) are useful in the clinical assessment, diagnosis and treatment of MS. | P Quality: 899.00 Length: 197 | P Quality: 899.00 Length: 197 |
| C Sequence 612 BP; 117 A; 215 C; 166 G; 114 T; | P Ratio: 5.257 Gaps: 1 | P Ratio: 5.257 Gaps: 1 |
| T used in the assessment, diagnosis and treatment of multiple sclerosis | P Percent Similarity: 86.802 Percent Identity: 86.802 | P Percent Similarity: 86.802 Percent Identity: 86.802 |
| P PT New human myelin basic protein and proteolipid protein variant(s) used in the assessment, diagnosis and treatment of multiple sclerosis | P PT New human myelin basic protein and proteolipid protein variant(s) used in the assessment, diagnosis and treatment of multiple sclerosis | P PT New human myelin basic protein and proteolipid protein variant(s) used in the assessment, diagnosis and treatment of multiple sclerosis |
| PT PT Claim 46; Page 110-112; 156pp; English. | PT PT Claim 46; Page 110-112; 156pp; English. | PT PT Claim 46; Page 110-112; 156pp; English. |
| PS PS A DNA construct (T41893) codes for MP4 chimera (W06103), a foetal protein composed of human myelin basic protein (MBP) foetal MBP21.5 (see also W00399) and delta PLP4 (W06101); a protein (PLP) protein that lacks all 4 hydrophilic domains of native human PLP (W06106) but includes PLP epitopes associated with multiple sclerosis (MS). It was constructed from DNA sequences encoding MPB21.5 (T4189) and delta PLP4 (T41891). The gene in vector PET22B was used to express MP4 in E. coli. W3110. The PLP polypeptides (see also W00400, W06101-02 and W06104-05) used in the clinical assessment, diagnosis and treatment of multiple sclerosis | PS PS A DNA construct (T41893) codes for MP4 chimera (W06103), a foetal protein composed of human myelin basic protein (MBP) foetal MBP21.5 (see also W00399) and delta PLP4 (W06101); a protein (PLP) protein that lacks all 4 hydrophilic domains of native human PLP (W06106) but includes PLP epitopes associated with multiple sclerosis (MS). It was constructed from DNA sequences encoding MPB21.5 (T4189) and delta PLP4 (T41891). The gene in vector PET22B was used to express MP4 in E. coli. W3110. The PLP polypeptides (see also W00400, W06101-02 and W06104-05) used in the clinical assessment, diagnosis and treatment of multiple sclerosis | PS PS A DNA construct (T41893) codes for MP4 chimera (W06103), a foetal protein composed of human myelin basic protein (MBP) foetal MBP21.5 (see also W00399) and delta PLP4 (W06101); a protein (PLP) protein that lacks all 4 hydrophilic domains of native human PLP (W06106) but includes PLP epitopes associated with multiple sclerosis (MS). It was constructed from DNA sequences encoding MPB21.5 (T4189) and delta PLP4 (T41891). The gene in vector PET22B was used to express MP4 in E. coli. W3110. The PLP polypeptides (see also W00400, W06101-02 and W06104-05) used in the clinical assessment, diagnosis and treatment of multiple sclerosis |
| SQ Sequence 1122 BP; 241 A; 354 C; 296 G; 231 T; | SQ Sequence 1122 BP; 241 A; 354 C; 296 G; 231 T; | SQ Sequence 1122 BP; 241 A; 354 C; 296 G; 231 T; |

125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysGln 141
 126 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 451 GGCCTCGTTCAGGGCCGCGCCTGGCGACTATTAATCTGTCAAAAGG 500
 141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
 501 CTCACAAAGGCCCTGATGCCAGGTACCTGTCCTCAAATTTCAAACTGG 550
 158 LysGlyArgAspPheArgSerGlySerProLeuAlaArgArg 171
 551 GCGGCCGTTGATAGCCGTTCTGGCTCTCCGATGGCTAGACGT 591

seq_name: N_Geneseq_36 :t41895

seq_documentation_block:

ID T41895 standard; DNA; 1476 BP.

AC T41895; 1997 (first entry)

DT DE MMOP4 chimera (MBP21.5-MOP-delta PLP4 fusion) DNA.

KW Proteolipid protein1; PLP; delta PLP4; myelin basic protein; MBP;

KW MBP21.5; multiple sclerosis; autoimmunity; diagnosis;

KW therapy; T-lymphocyte; T-cell; MMOP4 chimera;

KW myelin oligodendrocyte glycoprotein; MOG; ds.

OS Synthetic.

PN W09634622-A1.

PD 07-NOV-1995.

PF 22-APR-1996; US05611.

PR 02-MAY-1995; US-431648.

PR 02-MAY-1995; US-431644.

PR 02-JUN-1995; US-482114.

PA (ALEX-) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;

PI NYE SH, Pelfrey CM, Squinto SP, Wilkins JA;

DR WPI: 96-505898/50.

DR P-PSD; W06105.

PT New human myelin basic protein and proteolipid protein variant(s) - used in the assessment, diagnosis and treatment of multiple sclerosis

PT Claim 48; Page 115-117; 156pp; English.

CC A DNA construct (T41895) codes for MMOP4 chimera (W06105), a fusion protein composed of human myelin basic protein (MBP) foetal isoform MBP21.5 (see also W00399), the extracellular domain of human myelin oligodendrocyte glycoprotein (MOG) and delta PLP4 (W06101), a proteolipid protein (PLP) mutant that lacks all 4 hydrophobic domains of native human PLP (W06105) but includes PLP epitopes associated with multiple sclerosis (MS). It was constructed by inserting a sequence encoding the MOG moiety into MP4 chimera DNA (see also T41893) between the MBP and PLP derived sequences. The recombinant MMOP4 chimera can be expressed in bacterial cell hosts, PLP polyptides (see also W00400, W06101-03 and W06105) are useful in the clinical assessment, diagnosis and treatment of MS.

Sequence 1476 BP; 332 A; 434 C; 403 G; 307 T;

alignment_scores:

| | |
|----------------------------|--------------------------|
| Quality: 899.00 | Length: 197 |
| Ratio: 5.257 | Gaps: 1 |
| Percent Similarity: 86.802 | Percent Identity: 86.802 |

alignment_block: ..

US-09-218-277-12 x T41895 ..

Align seq 1/1 to: T41895 from: 1 to: 1476

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
 1 ATGGCCTCTGAAACGTCCTCCAGGTCAAGGTCCTCARATACTGGC 50
 17 arthralaserThreMetAspPhsAlaArgHisGlyPheLeuProArgHisA 34
 51 CACGCCAGCACCATGGACCATGGCCGTCATGGCTTCCTGGCCGCACCC 100

34 rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAsparg 50
 101 GTGACACCGCAtCTCGGACTCCATCGGGCTCTGGGGTACCTGGGACCGT 150
 51 GlyAlaProLysArgGlySerGly..... 58
 151 GGTGGGCCGAAACGTTGGCTCTGGCTGAACGGGGCG 200
 58 58
 201 TAGCCGGCTCCGTCATGCCSTAGGCCCTAGGCCGCGCTGTGGAACAGTG 250
 59 . LysAspSerHisHisProAlaArgThrAlaHistyrosLerLeuPro 74
 251 ACAARGACTCCACCCACCGGCTGTGTAACGGCCTAATGGCTCCCTGGCG 300
 75 GluLysSerHisGlyArgPheGlyAspGluAsnProValAlaHisPhePh 91
 301 CAGAAATCCACGGCGTACGCCAGATGAAACCGGGGGTGCACTTCTT 350
 91 eLysAsnIleValThrProArgGlyProArgProSerGlyGlyLysGlyA 108
 351 CAAARACATGTGACCCCCGTTACCCGCCGCTCTGGGAAAGGCC 400
 108 rgGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
 401 GTGGCTGTGCTCTGAGCCCTTCAGCTGGCTGGCAAGGCCACGTCGG 450
 125 GlyPheGlyArgGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG 141
 451 GGCCTCAGGTTACGGGGGGCTGGCTCCGACTTAAATCTGCTCACAAAGG 500
 141 YPhelGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
 501 CTTCAGGGCTGGATGCCAGGTACCTTGTCCAATTTCAAACTGG 550
 158 LysGlyArgAspSerArgSerGlySerPrometaLeuArgArg 171
 551 GCGCCGTTAGCGCTTCGGCTTCGGATGGCTAGACGT 591

seq_name: N_Geneseq_36:T41894

seq_documentation_block:

ID T41894 standard; DNA; 1125 BP.

AC T41894; 1997 (first entry)

DT DE PM4 chimera (delta PLP4-MBP21.5 fusion) DNA.

KW Proteolipid protein; Pur; delta PLP4; myelin basic protein; MBP;

KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;

KW therapy; T-lymphocyte; T-cell; PM4 chimera;

OS Synthetic.

PN W0934622-A1.

PD 07-NOV-1996.

PF 22-APR-1996; US05611.

PR 02-RAY-1995; US-431648.

PR 02-RAY-1995; US-431644.

PR 07-JUN-1995; US-482114.

PA (ALXH-) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;

PI NYE SH, Pelfrey CM, Squinto SP, Wilkins JA;

DR WPI: 96-505898/50.

DR P-PSD; W06105.

PT New human myelin basic protein and proteolipid protein variant(s) - used in the assessment, diagnosis and treatment of multiple sclerosis

PT Claim 48; Page 115-117; 156pp; English.

CC A DNA construct (T41894) codes for MMOP4 chimera (W06105), a fusion protein composed of human myelin basic protein (MBP) foetal isoform MBP21.5 (see also W00399), the extracellular domain of human myelin oligodendrocyte glycoprotein (MOG) and delta PLP4 (W06101), a proteolipid protein (PLP) mutant that lacks all 4 hydrophobic domains of native human PLP (W06105) but includes PLP epitopes associated with multiple sclerosis (MS). It was constructed by inserting a sequence encoding the MOG moiety into MP4 chimera DNA (see also T41893) between the MBP and PLP derived sequences. The recombinant MMOP4 chimera can be expressed in bacterial cell hosts, PLP polyptides (see also W00400, W06101-03 and W06105) are useful in the clinical assessment, diagnosis and treatment of MS.

Sequence 1476 BP; 332 A; 434 C; 403 G; 307 T;

PR 02-RAY-1996; US05611.

PR 02-RAY-1995; US-431648.

PR 02-RAY-1995; US-431644.

PR 07-JUN-1995; US-482114.

PA (ALXH-) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;

PI NYE SH, Pelfrey CM, Squinto SP, Wilkins JA;

DR WPI: 96-505898/50.

DR P-PSD; W06105.

PT New human myelin basic protein and proteolipid protein variant(s) - used in the assessment, diagnosis and treatment of multiple sclerosis

PT Claim 47; Page 113-114; 156pp; English.

CC A DNA construct (T41894) codes for PM4 chimera (W06104), a fusion protein composed of delta PLP4 (W06104) and MBP21.5 (W00399).

CC Delta PLP4 is a proteolipid protein (PLP) mutant that lacks all 4 hydrophobic domains of native human PLP (W06106) but includes PLP epitopes associated with multiple sclerosis (MS). MBP21.5 is a foetal isoform of human myelin basic protein (MBP) associated with

CC MS. The DNA was constructed from sequences encoding delta PLP4 (T41891) and msp21.5 (T41889). The gene fusion can be used to express PM4 in bacterial hosts. PLP polypeptides (see also W004004, CC W06101-03 and W06105) can be used in the clinical assessment, CC diagnosis and treatment of MS.

Sequence 1125 BP; 239 A; 359 C; 299 G; 228 T;

alignment_scores:

| | | | |
|---------------------|--------|-------------------|--------|
| Quality: | 894.00 | Length: | 196 |
| Ratio: | 5.259 | Gaps: | 1 |
| Percent Similarity: | 86.735 | Percent Identity: | 86.735 |

Align seg 1/1 to: 141894 from: 1 to: 1125

2 AlaserGlnLyArgProSerIlnArgHisGlySerLysTyrLeuAlaIth 18
 520 GCTCTCAGAAGCTGCCTCCAGCGTCACGCCCTAAATCTGCCAC 569

18 RAlaserThrMetAspIhsIlaArgHsIgLyPhelLeuProArgHsIArgA 35
 570 CCGAGACCATGGACCATGCCGTCATGGCTCCNGCGTCACCGTG 619

35 SPhrGlyIleLeuAspSerIleGlyArgPhelLeuProArgHsIArgA 51
 620 ACACCGGCAACGGGGC1CTGGACTCCATGGCCGCTTCGGGACCTGGT 669

52 AlaprolylArgGlySerGly 58
 670 GCGCCGAAACGGGGC1CTGGCAAAAGTCCGCTGAACCGGCCCTAG 719

59 1 59
 720 CCGGTCCGTTCATGCCGTAGCCAGCTGTGACACATGTACA 769

59 YsAspSerHsIHisProAlaArgThrAlaIstTyrGlySerIleProGln 75
 770 AGACTCCACCAACCCCGCTCTACCCCGCACTATGCTCCCTGCCAG 819

76 LysSerHsIlysGlyArgIhsGlnAspGluAsnProValHsIphePhely 92
 820 RAAATCCCACGGCGTACCCAGATGAAACCCGGTGTGCAATTCTCAA 869.

92 AsnIleValThrProArgThrProProSerProMetAlaArgArg 109
 870 AACATTTGACCCGGTACCCAGATGAAAGGGCGGT 919

109 IysLeuSerIleSerArgPheserTriPheIleAlaIgLyGlnArgProGly 125
 920 GCGTGTCCCTGACCCGGTTCACCTGGGGCCAGGCCAGCTCCGGC 969

126 PhgLyTyrgIgLyArgAlaSerAspTyrLysSerAlaIstLysGlyph 142
 970 TCTGGCTACGGGGCCGCGCCGCAATAATCTCTCTCAAAAGCTT 1019

142 ElysGlyvalAspAlaIgLyGlyThrIleSerIlePhelysLeuIiyG 159
 1020 CAAGGGCTGGATGCCAGGGACCCCTGTCAAAATTCAAAACTGGGG 1069

159 LyArgAspSerArgSerIgLySerProMetAlaArgArg 171
 1070 GCGGTGATAGCCGTTCTCGGCTCTCCGATGGCTAGACGT 1107

seq_name: N_Geneseq_36:Q48975

seq_documentation_block:

ID Q48975 standard; cDNA to mRNA; 1147 BP.

AC Q48975;

DT 18 APR 1994 (first entry)

DE Encodes RB35 protein from rat brain.

KW RB35 antigen; immunogen; myelin; Sprague-Dawley; rat; brain;

KW antibody; IgG1; ds.

OS Rattus norvegicus (Sprague-Dawley).

PN J05219982-A.

PD 31 AUG 1993.

PF 07-AUG-1992; 055983.

PR 07-FEB-1992; JP-055983.

PA (TOKE) TOSHIBA KK.

DR 93-308342/39.

PT Monoclonal antibody against the proteins distributed in the brain

- is prep. by using rat brain extract as immunogen belonging to

PT IgG1 class which combines to rat brain extract antigen

Claim 2; Page 2-3; 16pp; Japanese.

The sequence coding for RB35 was isolated from a cDNA library

CC prepared from total adult female Sprague-Dawley rat brain mRNA.


```

SQ Sequence 63 BP; 21 A; 16 C; 7 G; 19 T;
alignment_scores:
    Quality: 107.00 Length: 19
    Ratio: 5.632 Gaps: 0
    Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x T67170 ..
Align seg 1/1 to: T67170 from: 1 to: 63
  83 AspGluAsnProValAlaHisPhePheLeuAsnIleValThrProArgTh 99
  ||||||| | | | | | | | | | | | | | | | | | | | | | | | | |
  5 GATTAATTCAGTAGTTCATTTTAAATAATGTAAACCCACGTAC 54
  99 rppro 101
  ||||| |
  55 CCACCC 61

seq_name: N_Geneseq_36:T67171

seq_documentation_block:
ID T67171 standard; DNA; 63 BP.
AC T67171_
DT 19-FEB-1998 (first entry)
DE Human BPP-PE chimeric protein construction oligonucleotide Oligo 5
KW Pseudomonas exotoxin; myelin basic protein; chimeric protein;
KW autoimmune disease; multiple sclerosis; human; ss.
KW Synthetic.
OS Homo sapiens.
OS WO719179-A1.
PD 29-MAY-1997.
PD 17-NOV-1996; IL-0151.
PR 26-DEC-1995; IL-116559.
PR 17-NOV-1995; IL-116044.
PA (YISS ) YISSUM RES & DEV CO.
PI Berraud E, Lherbouy-Gaiski H, Marianovsky I, Steinberger I;
PI Yarkoni S;
PR WP; 97/298116/27.
PT New Pseudomonas exotoxin-myelin basic protein chimeric proteins -
PT used for the treatment of auto-immune diseases, particularly
PT multiple sclerosis
PS Claim 7; Page 22; 54pp; English.
CC New chimeric proteins have been developed comprising a Pseudomonas
CC aeruginosa exotoxin (PE) moiety linked to a myelin basic protein (MBP)
CC moiety selected from: (a) MBP; (b) amino acids 69-88 of quinea-pig
CC or an antigenic portion; (c) amino acids 84-102 of human MBP or an
CC antigenic portion; (d) amino acids 143-168 of human MBP or an amino
CC portion; and (e) an amino acid sequence in which one or more amino
CC acids have been deleted, added, substituted or mutated in the amino acid
CC sequences of (a), (b), (c), or (d), the modified sequences retaining
CC at least 75% homology with the amino acid sequences. The present seqn
CC represents an oligonucleotide used for constructing human BPP-PE
CC chimeric proteins. The chimeric proteins can be used for the treat-
CC of autoimmune diseases such as multiple sclerosis. The chimeric pro-
CC teins can specifically target and kill MBP specific T cells while having
CC no effect on non-target cells.
SQ 63 BP; 21 A; 15 C; 8 G; 19 T;

alignment_scores:
    Quality: 107.00 Length: 19
    Ratio: 5.632 Gaps: 0
    Percent Similarity: 100.000 Percent Identity: 100.000

```


ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30-399
 REFERENCE/DOCKET NUMBER: ALX-129
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (203) 254 1101
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 519 base pairs
 TYPE: Nucleic acid
 STRANDEDNESS: Double
 TOPOLogy: Linear
 MOLECULE TYPE: cDNA to mRNA
 DESCRIPTION: Human 18.5 kDa form of MBP
 HYPOThETICAL: No
 ANTI-SENSE: No
 PCT-US96-05611A-4

seq_name: /cgnl_7/prodate/v1/lna/PCNUS_COMB.seq: PCT-US96-05611A-4

seq_documentation_block:

Sequence 4, Application PC/US9605611A
 GENERAL INFORMATION:
 APPLICANT: Mueller, John P.
 APPLICANT: Lenardo, Michael J.
 APPLICANT: McFarland, Henry F.
 APPLICANT: Matis, Louis A.
 APPLICANT: Mueller, Eileen Elliott
 APPLICANT: Nye, Steven H.
 APPLICANT: Pelfrey, Clara M.
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Wilkins, James A.
 TITLE OF INVENTION: Modified Myelin Protein Molecules
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maurice M. Klee
 STREET: 1951 Burr Street
 CITY: Fairfield
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06430

COMPUTER READABLE FORM:
 COMPUTER TYPE: 3.5 inch, 0.8 Mb storage
 OPERATING SYSTEM: Macintosh Centris 610
 SOFTWARE: System 7
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/05611A
 FILING DATE: 02-MAY-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/431, 644
 FILING DATE: MAY 2, 1995
 APPLICATION NUMBER: 08/431, 648
 FILING DATE: MAY 2, 1995
 APPLICATION NUMBER: 08/482, 114
 FILING DATE: June 7, 1995

Maurice Klee

101 GAGACGGGATCCTTGACTCCATCGGGCCTCTTGGGGTACAGG 150
 51 GlyAlaProLysArgGlySerGlyLysAsnSerHisSerHisProAlaArgTh 67
 151 GGTGCCCAAGGGGCTCGGAGGACTCACACCCACGGCAAGAAC 200
 67 RalaHistYrglySerLeuProGlyLysSerHisGlySerHisProAlaArgTh 84
 201 TGTCGACTATGGCTCCCTGCCAGAGTCACACGCCGACCGAGATG 250
 84 LusnProValHsPheHsAsnLeuThrProArgThPro 100
 251 AAACCCCGTAGTCCTCTCAAGAACATGTGAGCCCTGCACCA 300
 101 ProProSerGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTh 117
 301 CCCCGTCGAGGGAAAGGGAGGAGCTCAAGGAGATCGAGGCCAGG 350
 117 pglyAlaLuglyGlyGlyLuglyGlyLeuSerLeuSerArgPheSerTh 134
 351 GGGGCCGAAGGCCAGAGGACCATGGCTACGGAGGAGGGCTCG 400
 134 SPTYLYSSTlePhaLysLeuGlyGlyArgGlyLysSerArgSerGlySe-Pr 150
 401 ACTATAATCGCTCAAGGATTCAGGAGTCATGCCAGGCCAG 450
 151 LeuSerLysStlePhaLysLeuGlyGlyArgGlyArgSerArgSerGlySe-Pr 167
 451 CTTTCGAAATTTAAGCTGGAGGAGAGATGCGCTCGTGCACCA 500
 167 ometLaargArg 171
 501 CATGGCTAGAGCC 513

alignment_scores:
 Quality: 922.00 Length: 171
 Ratio: 5.392 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: PCT-US96-05611A-4 from: 1 to: 519

1 MetAlaSerGlnLysArgProSerGlnArgLysGlySerLysTyroLeuAl 17
 4 ATGGGGTCACAGAGAGACCCCTCCAGAGGCAAGTCAAGTGCACCG 53

17 atmAlaSerThrMetAspHisAlaArgRhsGlyPheLeuProArgHsA 34
 54 CACAGCAGAAGTACATGGACCATGCCAGGATGCGCTCCGCCAGGCACA 103

34 RgAPtHgLyIleLeuAspSerLeuAspSerGlyArgPhePheDlyGlyAspArg 50

104 GAGACACGGGCATCTGACTCCATCGGGCCTCTTGGGCTGACAGG 153

51 GlyAlaProLysArgGlySerGlyLysAsnSerHisProAlaArgTh 67
 154 GTGGCCCAAGGGCTCTGCAAGGACTCACACCCGGCAGAAC 203

67 RalaHistYrglySerLeuProGlyLysSerHisGlyArgGlyLysGly 84
 204 TGTCGACTATGGCTCCCTGCCAGAGCTCAAGGAGATCGAGGCCAGG 253

84 LusnProValHsPheHsAsnLeuThrProArgThPro 100
 254 AAACCCCGTAGTCCTCTCAAGAACATGTGAGCCCTGCACCA 303

101 ProProSerGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTh 117
 304 CCCCGTCGAGGGAAAGGGAGGAGCTCAAGGAGATCGAGGCCAGG 353

117 pglyAlaLuglyGlyGlyLuglyGlyLeuSerLeuSerArgPheSerTh 134
 354 GGAGCCGAGGGCAAGGAGGAGCTCAAGGAGATCGAGGCCAGG 403

134 SPTYLYSSTlePhaLysLeuGlyGlyArgGlyLysSerArgSerGlySe-Pr 150
 404 ACTATAATCGCTCAAGGAGATCGAGGCCAGGAGCTCAAGGAG 453

151 LeuSerLysStlePhaLysLeuGlyGlyArgGlyLysSerArgSerGlySe-Pr 167
 454 CTTCGAAATTTAAGCTGGAGGAGAGATGCGCTCGTGCACCA 503

167 ometLaargArg 171
 504 CATGGCTAGAGCC 516

seq_name: /cgnl_7/podata/1/ina/pctus_comb.seq:pct-US96-05611A-1

; Sequence 1, Application block:

; GENERAL INFORMATION:

APPLICANT: Mueller, John P.

APPLICANT: Lenardo, Michael J.

APPLICANT: McFarland, Henry F.

APPLICANT: Matis, Louis A.

APPLICANT: Mueller, Eileen Elliott

APPLICANT: Nye, Steven H.

APPLICANT: Peifrey, Clara M.

APPLICANT: Squinto, Stephen P.

TITLE OF INVENTION: Modified Myelin Protein Molecules

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESS: Maurice M. Klee

STREET: 1951 Burr Street

CITY: Fairfield

STATE: Connecticut

COUNTRY: USA

ZIP: 06430

CURRENT APPLICATION DATA:

FILING DATE: 02-MAY-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/431,644

FILING DATE: May 2, 1995

APPLICATION NUMBER: 08/431,648

FILING DATE: May 2, 1995

APPLICATION NUMBER: 08/482,114

FILING DATE: June 7, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Klee, Maurice M.

REFERENCE DOCKET NUMBER: ALX-129

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203) 255 1400

TELEFAX: (203) 254 1101

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 594 base pairs

TYPE: Nucleic acid

STRANDEDNESS: Double

TOPOLOGY: Linear

MOLECULE TYPE: cDNA to mRNA

DESCRIPTION: MBP-X2Cys81/hum. (Human 21.5 kd form

HYPOTHETICAL: No

ANTI-SENSE: No

PUBLICATION INFORMATION:

AUTHORS: Roth, R. J.

AUTHORS: Kronquist, K. E.

AUTHORS: Keeler de Rosbo, N.

AUTHORS: Crandall, B. F.

AUTHORS: Campagnoni, A. T.

TITLE: Evidence for the Expression of Four

TITLE: Myelin Basic Protein Variants in the

TITLE: Developing Human Spinal Cord Through

JOURNAL: CDNA Cloning

JOURNAL: Journal of Neuroscience Research

PAGES: 312 - 328

DATE: 1987

PCT-US96-05611A-1

alignment_scores:

Quality: 899.00

Length: 197

Ratio: 5.257

Gaps: 1

Percent Similarity: 86.802

Percent Identity: 86.802

alignment_block:

US-09-218-277-12 x PCT-US96-05611A-1 ..

Align seg 1/1 to: PCT-US96-05611A-1 from: 1 to: 594

~ 1 MetAlaserGlnLysArgProSerGlnArgHisGlySerLysTyrLeuI

1 ATGGCGTCACAGANGAGACCCCTCCAGAGGCACGGATCCAAGTACGTGCC

17 aThrLaserThrMetAspHisAlaArgHisGlyPheLeuProArgHisA

51 CACAGCAAGGACCTCTGACTCATCGGCCCTCTGGCTAACCGGGCCG

34 rGaspThrGlyLeuAspPserLysGlyArgPheLeuGlyAspArg

101 GAGAGACGGGCCACCTGACTCCATCGGCCCTCTGGCTAGGCAAG

51 GlyAlaProLysArgGlySerGly.....

58 .LysAspSerHistisProAlaArgThrAlaHistYsLysSerLeuPro

75 GluLysSerHisGlyArgThrGlyLysGluAsnProValValHisPheP

91 ACAGAGACTCACACACCACCGCGCAGAACTGCTCACTATGCCCTGCC

251 ACAAGACTCACACACCACCGCGCAGAACTGCTCACTATGCCCTGCC

75 GluLysSerHisGlyArgThrGlyLysGluAsnProValValHisPheP

91 elysasnilevalhrProArgThrProProProSerGlyGlyGlyA

351 CAAGACATTTGAGCCGCTCGACACCCCGCTCGAGGGAAAGGGAA

108 rGlyLysLeuSerLeuSerArgTrpHeSerTrpGlyAlaLysGluGlyLysGly

125 GlyPheGlyTrpGlyGlyArgAlaSerAspTrpLysSerAlaHisLysG

451 GGATTTGGCTACGGAGGCGAGGCGTCCGACTATAATCGGCTCACAGGG

141 PheArgGlyValAspAlaGlyLysGlyThreIleSlysIlePhePheLysLeu

501 ATTCAAGGGAGTCatGCCAGGGCACGTTTCAAATTCAGCTGG

158 LysLysArgAspSerArgSerGlySerProLeuIleArg

551 GAGGAGAGAGTAGCGCTCGATCACCAAGGCTAGAGGC

591

seq_name: /cgnl_7/podata/1/ina/pctus_comb.seq:pct-US96-05611A-2

; seq_documentation_block:

; Sequence 2, Application PC/TU9605611A

; GENERAL INFORMATION:

APPLICANT: Mueller, John P.

APPLICANT: Lenardo, Michael J.

APPLICANT: McFarland, Henry F.

APPLICANT: Matis, Louis A.

APPLICANT: Mueller, Eileen Elliott

APPLICANT: Nye, Steven H.

APPLICANT: Peifrey, Clara M.

APPLICANT: Squinto, Stephen P.

APPLICANT: Wilkins, James A.
 TITLE OF INVENTION: Modified Myelin Protein Molecules
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Maurice M. Klee
 STREET: 1951 Burr Street
 CITY: Fairfield
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06430
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
 COMPUTER: Macintosh Centris 610
 OPERATING SYSTEM: System 7
 SOFTWARE: Microsoft Word 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US96/05611A
 FILING DATE: 02-MAY-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/431,644
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/431,648
 FILING DATE: May 2, 1995
 FILING DATE: June 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30,399
 REFERENCE/DOCKET NUMBER: ALX-129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (03) 255 1400
 TELEFAX: (203) 254 1101
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 612 base pairs
 TYPE: Nucleic acid
 STRANDEDNESS: Double
 TOPOLOGY: Linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: MBP+xCys81/bact.
 HYPOTHETICAL: No
 ANTI-SENSE: No
 PCT-US96-05611A-2

alignment_scores:
 Quality: 899.00 Length: 197
 Percent Similarity: 5.257 Gaps: 59.1
 Percent Identity: 86.802

alignment_block:
 US-09-218-277-12 x PCT-US96-05611A-2 ..

Align seg 1/1 to: PCT-US96-05611A-2 from: 1 to: 612

seq_name: /cgn1_7/ptodata/1/lna/PCTUS_COMB.seq; PCT-US96-05611A-3
 seq_documentation_block:
 ; Sequence 3, Application PC/US96/05611A
 ; General Information:
 ; APPLICANT: Mueller, John P.
 ; APPLICANT: Lenardo, Michael J.
 ; APPLICANT: McFarland, Henry F.
 ; APPLICANT: Mattis, Louis A.
 ; APPLICANT: Mueller, Eileen Elliott
 ; APPLICANT: Nye, Steven R.
 ; APPLICANT: Peffrey, Clara M.
 ; APPLICANT: Squinto, Stephen P.
 ; APPLICANT: Wilkins, James A.
 ; TITLE OF INVENTION: Modified Myelin Protein Molecules
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Maurice M. Klee
 ; STREET: 1951 Burr Street
 ; CITY: Fairfield
 ; STATE: Connecticut
 ; COUNTRY: USA
 ; ZIP: 06430
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
 COMPUTER: Macintosh Centris 610
 OPERATING SYSTEM: System 7
 SOFTWARE: Microsoft Word 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US96/05611A
 FILING DATE: 02-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/431,644
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/431,648
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/482,114
 FILING DATE: June 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30,399

201 TAGCCCGCTGCGGTCTCATGCCGGTACCCAGCCGGGCTGTCACATGT 250
 59 . LysaspSerHISProAlaArgThrAlaIstYrglySerLeuPro 74
 1 ATGGCGCTCTCAGAAAGTGTCGTCGGCCAGGTCAATTACCGGC 50
 17 athralaserthMetaphisAlaGluGlySerLysTyrLeu 17
 51 CACGCCAGCACCATGGACCATCCCCGTCATGGCTCTGGCCGTCACC 100
 34 rAspPArgGlyLysLeuLysPserLleGlyArgPhePheGlyGlyAspArg 50
 101 GTGACACGGCATCTGGACTCATCGGCCGCTTCGGCGTGACCGT 150
 51 GlyAla-PolySArgGlySerGly. 58
 151 GSPGCGCCGAAGCTGGCTGCTGCCAACGGGCGC 200

REFERENCE/DOCKET NUMBER: ALX-129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 254 1101
 FAX: (203) 254 1101

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 612 base pairs
 TYPE: Nucleic acid
 STRANDEDNESS: Double
 TOPOLOGY: Linear
 MOLECULE TYPE: cDNA to mRNA
 DESCRIPTION: MBP+X2SP181/3act.
 HYPOTHETICAL: No
 ANTI-SENSE: No
 PCT-US96-05611A-3

alignment_scores:

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|---------------------|--------|-------------------|--------|
| Quality: | 899.00 | Length: | 197 |
| Ratio: | 5.257 | Gaps: | 1 |
| Percent Similarity: | 86.802 | Percent Identity: | 86.802 |

alignment_block:

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Align seg 1/1 to: PCT-US96-05611A-3 from: 1 to: 612

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 1 ATGGCGTCAGAAAGTCCAGCGTCCAGCGTCACGGCTCCAAATCTGGC 50

17 athrilaaserThrMatAspHisAlaRArgHsGlySerlySryLeuProAghisa 34
 51 CACCCGAGCACCATGGACCATGGCCGTCAATGGCTTCCTGCCGCGTCACC 100

34 IqASpThrglyIleuAsSerIleGlyArgPhePheHgylGlyIasparg 50
 101 GTGAGACCGSCATCTGGACTTCATGGCGCTTCCTGCCGCGTCACC 150

51 GlyAlaProlysArgLySargly..... 58
 58

151 GGTGGCCGAGACGGCTTGCAAGTGGCTGTGAAACGGGGCG 200

58

201 TAGCCCGCTCGCTCATGCCGTAGCCAGCGGGCTGTGCAACATGT 250

59 .LysAspSerHisIshProLaagThrlahIHiTyrglySerIeupro 74
 251 ACAAAAGACTCCACCAACCGGGCTTACCGGCATAATGCCCTGGCG 300

75 GlntIrrSerHisIshArgThrgInaspGluasnPrvalWihIshpheph 91

301 CAGAAATCCAGGGTACCCAGGATGAAKACCGGGGGCACTCTT 350

108 RGLILLeuseLeuseArPheSeTrpGlyAlaGluglyGlnAlaPro 124

401 GTGGCGCTGCTCTGAGCGGTTCACTGGCGCGGAAGGCCAGGGCTT 450

125 GlyPheGlyTyrglylIyArgAlaSerAspMyrlylSerAlaHiLysgl 141

451 GCCTCGGTRAGGGCCGCTGGCGCTACCCGCCGCGTCAGGGCAAAGGCC 500

501 CTCAAGGGCGTGGATGCCAGGGTACCTGTCCTAACATTTCACAATGG 550

158 IYGLILArgAspSerArgSerIlySerProMetAlaRgarg 171

551 CGGCCGCGTATGCCGTTCTGCCATGGCTAGACGT 591

seq_name: /cgnl_7/pttodata/1/lna/PCTUS_COMB.seq:PCT-US96-05611A-26

seq_documentation_block:

sequence 26, application PC/TUS9605611A

GENERAL INFORMATION:

APPLICANT: Mueller, John P.
 APPLICANT: Lenardo, Michael J.
 APPLICANT: McFarland, Henry F.
 APPLICANT: Matis, Louis A.
 APPLICANT: Mueller, Eileen Elliott

APPLICANT: Nye, Steven H.
 APPLICANT: Pelfrey, Clara M.
 APPLICANT: Squinto, Stephen A.
 APPLICANT: Wilkins, James A.

TITLE OF INVENTION: Modified Myelin Protein Molecules

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maurice M. Klee

STREET: 1551 Burr Street

CITY: Fairfield

STATE: Connecticut

COUNTRY: USA

ZIP: 06430

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 0.8 Mb storage

COMPUTER: Macintosh Centris 610

OPERATING SYSTEM: System 7

SOFTWARE: Microsoft Word 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/05611A

FILING DATE: 02-MAY-1995

CATEGORIZATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/431,644

FILING DATE: May 2, 1995

APPLICATION NUMBER: 08/431,648

FILING DATE: May 2, 1995

APPLICATION NUMBER: 08/482,114

FILING DATE: June 7, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Klee, Maurice M.

REGISTRATION NUMBER: 30,399

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203) 254 1100

TELEFAX: (203) 254 1101

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 1122 base pairs

TYPE: Nucleic acid

STRANDEDNESS: Double

TOPOLOGY: Linear

MOLECULE TYPE: Other nucleic acid

DESCRIPTION: MP4 chimera

HYPOTHETICAL: No

PCT-US96-05611A-26

alignment_scores:

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|---------------------|--------|-------------------|--------|
| Quality: | 899.00 | Length: | 197 |
| Ratio: | 5.257 | Gaps: | 1 |
| Percent Similarity: | 86.802 | Percent Identity: | 86.802 |

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 17 athrAlaserThrMetaphsialaIargHslyPheleuProArhisa 34
 51 CACCGCCAGCACATGGACCATGCCGTCAATGCCGCTCTGCCGCGTCACC 100
 34 rgasPthrglyIleuAspSerIleuArgPhePheGlyIyAsparg 50
 101 GTGACACGGCAGTCTGGACTCATGCCGCTCTGCCGCGTGAACCGT 150
 51 GlyAlaProLyArgIyGlySerGly... 58
 151 GGRCGCAGAACGTTGCTGCAAGTGCCGTGAAACGGCGCG 200
 58 ... 58
 201 TAGCCGCTGCGCTCATGCCGTACGCCAGCGGGCTGTCACATGT 250
 59 . LysAspSerHisIyProAlaArgThrAlaHistyrglySerLeupro 74
 251 ACRAAGACTCCCACCCACCGGCTGTAACGCCGACTAAGGCTCCGCCG 300
 75 GlyLyserHsIyIyArgThrglyIyAspGluAsnProValAlaHisPhePh 91
 301 CAGAAATCCACAGCCGTAACCCAGGATGAAACCGGTTGCACTTCTT 350
 91 elysAsnIlevalThrProArgThrProProProSerGlyLysIyA 108
 351 CAAAACATTGACCCCGGTAACCCGGCCGCTCTCAGGCCAAGGCC 400
 108 rgyIyLeuSerIeuaSerArgPheSerItpgIyAlaIuglyIyInApro 124
 401 GIGGCCCTGCTCCCTGAGCGGTTAGCTGGGGCCGAGGCCAGCTCCG 450
 125 GlyPheGlyTyryglyIyArgAlaserAspTyrylyserAlaHistyrgly 141
 451 GGCTCGGTTACGGCCGCGTGCCTCCGACTATAATCTGCTCACAAAGG 500
 141 yPhelysGlyValAspAlaIagIyGlyIyLeuSerIyIlePhelysIeu 158
 501 CTTCACAAGGCGGTTGATGCCAGGGTACCTTGTCCAATTTCAACTGG 550
 158 lysIyArgAspSerArgSerGlySerProMetAlaIarg 171
 551 GCGGCCGTTAGCCGTCCTGGCTCTCCGATGGCTTACAGCT 591
 seq_name: /cgn1_7/pctodata/1/ina/PCTUS_COMB.seq: PCT-US96-05611A-25
 seq_documentation_block:
 Sequence 25, Application PC/US9605611A
 GENERAL INFORMATION:
 APPLICANT: Mueller, John P.
 APPLICANT: Lenardo, Michael J.
 APPLICANT: McFarland, Henry F.
 APPLICANT: Matis, Louis A.
 APPLICANT: Mueller, Eileen Elliott
 APPLICANT: Nye, Steven H.
 APPLICANT: Pelfrey, Clara M.
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Wilkins, James A.
 TITLE OF INVENTION: Modified Myelin Protein Molecules
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maurice M. Klee
 STREET: 1951 Burr Street
 CITY: Fairfield
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06430
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 0.8 mb storage
 COMPUTER: Macintosh Centris 610
 OPERATING SYSTEM: System 7

SOFTWARE: Microsoft Word 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/05611A
 FILING DATE: 02-MAY-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/431,644
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/431,648
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/482,114
 FILING DATE: June 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30,399
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 255 1400
 TELEFAX: (203) 254 1101
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1155 base pairs
 TYPE: Nucleic acid
 STRANDEDNESS: Double
 TOPOLOGY: Linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: MP3 chimera
 HYPOTETICAL: No
 ANTI-SENSE: No
 PCT-US96-05611A-25

alignment_scores:
 Quality: 899.00 Length: 197
 Percent Similarity: 5.257 Gaps: 1
 Percent Identity: 86.802 Percent Identity: 86.802

alignment_block:
 US-09-218-277-12 x PCT-US96-05611A-25 ..

Align seg 1/1 to: PCT-US96-05611A-25 from: 1 to: 1155

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 34 rgasPthrglyIleuAspSerIleuArgPhePheGlyIyAsparg 50
 101 GTGACACGGCAGTCTGGACTCATGCCGCTCTGCCGCGTGAACCGT 150
 51 GlyAlaProLyArgIyArgIy... 58
 151 GGTCGCGCAAGGCGCTCTGGCAAGTGCCGTGAAACGGCCG 200
 58 ... 58
 201 TAGCCGCTGCGCTCATGCCGTAGCCGCTGTCACATGT 250
 59 . LysAspSerHisIyProAlaArgThrAlaHistyrglySerLeupro 74
 301 CAGAAAGACTCCCACCCGGCTGTAACGCCGACTATGCTCCGCCG 300
 75 GlyLyserHsIyIyArgThrglyIyAspGluAsnProValAlaHisPhePh 91
 301 CAGAAATCCACAGCCGCTGTAACCCAGGATGAAACCCGGGTTGCACTT 350
 91 elysAsnIlevalThrProArgThrProProProSerGlyIyLysIyA 108
 351 CAAAACATTGACCCGGTACCCGCCGCGTCTCAGGCCAAGGCC 400.

PCT-US96-05611A-28

108 rgglyleuserLeuserArgPheserTrpglyAlaGluGlyGlnArgPro 124
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 401 GTCGGCTGTCCTGAGCCCTTCACTGGGGCCGGAAAGGCCAGGTCGG 450

125 GlpHeGlyTyrglyLygargalaserAspTyrLysSerAlaLysLysGly 141
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 451 GGCCTCGGTTACGGGGCGCTGGTCCACTATAATGTCACAAAGG 500

141 YphelysGlyValAspAlaGlyLysThrLeuserLysIlePheLysLeug 158
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501 CTCRAAGCGGTGATGCCAGGGTACCTGTGCCAARATTCAACTGG 550
 158 LygIyArgAspSerArgSerGlySerPrometaLaArgArg 171
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 551 GCGGCGTGTAGCCTCTGGCTCCATGGTAGAGCT 591

seq_name: /egnl_7/pctoata/1/ina/PCUS_COMB.seq:PCT-US96-05611A-28
 seq_documentation_block:
 sequence 28, Application PC/TUS9605611A

; GENERAL INFORMATION:
 ; APPLICANT: Mueller, John P.
 ; APPLICANT: Lenardo, Michael J.
 ; APPLICANT: McFarland, Henry F.
 ; APPLICANT: Matis, Louis A.
 ; APPLICANT: Mueller, Eileen Elliott
 ; APPLICANT: Nye, Steven H.
 ; APPLICANT: Pelfrey, Clara M.
 ; APPLICANT: Squinto, Stephen P.

APPLICANT: Wilkins, James A.
 TITLE OF INVENTION: Modified Myelin Protein Molecules
 NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maurice M. Klee

STREET: 1951 Burr Street
 CITY: Fairfield
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06430

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 Inch, 0.8 Mb storage
 COMPUTER: Macintosh Centris 610
 OPERATING SYSTEM: System 7
 SOFTWARE: Microsoft Word 6.0.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/05611A
 FILING DATE: 02-May-1995
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/431,644
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/431,648
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/482,114
 FILING DATE: June 7, 1995

ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30,399
 REFERENCE/DOCKET NUMBER: ALX-129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 255 1400
 TELEFAX: (203) 254 1101
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1476 base pairs
 TYPE: Nucleic acid
 STRANDBNESS: Double
 TOPOLOGY: Linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: MMGMP4 chimera
 HYPOTHETICAL: No
 ANTI-SENSE: No

alignment_scores:
 Quality: 899.00
 Ratio: 5.25/
 Percent Similarity: 86.802
 Length: 197
 Gaps: 1
 Percent Identity: 86.802

alignment_block:
 US-09-218-277-12 x PCT-US96-05611A-28
 ..

Align seg 1/1 to: PCT-US96-05611A-28 from: 1 to: 1476

1 MetAlaSerGlyLysAsgProSerGinArgHsGlySerLysTyrLeual 17

1 AUGCGCTCAAAACGAGGCGCCAGGTCAGGCCAAATACCGGGC 50

17 atmAlaSerLysMetaphisAlaArgHsGlyPhalaProArRisa 34
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 51 CACGGCCAGCACCATGGACCATGGCCAGCCGTCAGCTCTTGCGCGTACCC 100

34 rgasprhglyleuAspSerIleGlyArgPhpheGlyAspArg 50
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 101 GTGACACCGGCACTCTGGACTCATCGCCGCTCTGGGGTGACCGT 150

51 GlAlaProLySArgGlySerGly..... 58

151 GTGCGCCGAAGGTGGCTCGCAAGTGCGTGAACCGGGCCG 200

58 58

201 TAGCCCGCTGCCCTCTCTGCCCCGTAGCCAGCGGGCTGICCAACATGT 250

59 . LysAspSerHisSerHisProAlaArgHsAlaHistYrgLysSerLePro 74

251 ACRAAGACCTCCACCAACCGGGCTGTAACGGCCACTATGGCTCCCTGGG 300

75 GlNlysSerHisGlyArgThrgInAspGluAsnProValValHisPhePh 91

301 CAAACATGCCAGGCCGACCAGGAGGAACCCGCTGGTCACTCTT 350

91 eLysAsnIleValThrProAlaArgThrProProProSerGlnGlyLysGly 108

351 CAAACATGACCCCGAACCCGCCGCTCAGGGCAAGGCC 400

108 rgglyleuserLeuserArgPheserTrpglyAlaGluGlyGlnArgPro 124

401 GTCGGCTGTCCTGAGCTGGGGGGGAGGCCAGCGTCGG 450

125 GlpHeGlyTyrglyLygargalaserAspTyrLysSerAlaLysGly 141
 ||||| ||||| ||||| ||||| ||||| ||||| |||||

451 GGCCTCGGTTACGGGGCGCTGGTCCACTATAATGTCACAAAGG 500

141 YphelysGlyValAspAlaGlyLysThrLeuserLysIlePheLysLeug 158
 ||||| ||||| ||||| ||||| ||||| |||||

501 CTCRAAGCGGTGATGCCAGGGTACCTGTGCCAARATTCAACTGG 550

158 LygIyArgAspSerArgSerGlySerPrometaLaArgArg 171
 ||||| ||||| ||||| ||||| ||||| |||||

551 GCGGCGTGTAGCCTCTGGCTCTCGATGCTAGAGCT 591

seq_name: /egnl_7/pctoata/1/ina/PCUS_COMB.seq:PCT-US96-05611A-27
 seq_documentation_block:
 sequence 27, Application PC/TUS9605611A

; GENERAL INFORMATION:
 ; APPLICANT: Mueller, John P.
 ; APPLICANT: Lenardo, Michael J.
 ; APPLICANT: McFarland, Henry F.
 ; APPLICANT: Matis, Louis A.
 ; APPLICANT: Mueller, Eileen Elliott
 ; APPLICANT: Nye, Steven H.
 ; APPLICANT: Pelfrey, Clara M.

APPLICANT: Squinto, Stephen P. 59
 APPLICANT: Wilkins, James A.
 TITLE OF INVENTION: Modified Myelin Protein Molecules
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maurice M. Klee
 STREET: 1951 Burr Street
 CITY: Fairfield
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06430

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
 COMPUTER: Macintosh Centris 610
 OPERATING SYSTEM: System 7
 SOFTWARE: Microsoft Word 6.0.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/05611A
 FILING DATE: 02 MAY -1995
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/431, 644
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/431, 548
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/482, 114
 FILING DATE: June 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30, 399
 REFERENCE/DOCKET NUMBER: AIX-129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 255 1400
 TELEFAX: (203) 254 1101

SEQUENCE CHARACTERISTICS: 27:

LENGTH: 1125 base pairs
 TYPE: Nucleic acid
 STRANDEDNESS: Double
 TOPOLOGY: Linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: PM4 chimera
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 PCT-US96-05611A-27

alignment_scores:
 Quality: 894.00 Length: 196
 Ratio: 5.259 Gaps: 1
 Percent Similarity: 86.735 Percent Identity: 86.735

alignment_block:
 US-9-218-277-12 x PCT-US96-05611A-27 ..

Align seq 1/1 to: PCT-US96-05611A-27 from: 1 to: 1125

2 AlaSerGlnLysArgProSerGlnIgArgLysGlySerLysLeuIalath 18
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 520 GCGTCAGAAACGGCTCCAGGTCAACCTGGCAC 569

35 SphThrGlyIleLeuAspSerIleGlyArgPhePheIgLyAsparGly 51
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 620 ACACCGCAGCATCTGGACTCCACGGCGCTTCTGGGGTGACCGGTG 669

52 AlaProLySArgGlyArgGly..... 58
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 670 GCGCCCAAAGTGGCTCTGGAAAGGCCGGCTAACGGGGCGTAG 719

seq_name: /cgn1_7/ptodata/1/ina/PCTUS.seq:PCT-US96-05611A-8
 seq documentation block:
 Sequence 8, Application PCT/US96/05611A
 GENERAL INFORMATION:
 APPLICANT: Mueller, John P.
 APPLICANT: Lenardo, Michael J.
 APPLICANT: McFarland, Henry F.
 APPLICANT: Matis, Louis A.
 APPLICANT: Mueller, Eileen Elliott
 APPLICANT: Nye, Steven H.
 APPLICANT: Pelfrey, Clara M.
 APPLICANT: Squinto, Stephen P..
 APPLICANT: Wilkins, James A.
 TITLE OF INVENTION: Modified Myelin Protein Molecules
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maurice M. Klee
 STREET: 1951 Burr Street
 CITY: Fairfield
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06430

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
 COMPUTER: Macintosh Centris 610
 OPERATING SYSTEM: System 7
 SOFTWARE: Microsoft Word 6.0.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/05611A
 FILING DATE: 02 MAY -1995
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/431, 644
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/431, 548
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/482, 114
 FILING DATE: June 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.

59
 720 CCCGTGCCCTCTATGCCGGTAGGCCAGCCGGCCTGGCAACATGTACA 769
 59 YsAsPserHishisroAlaArgThrAlaHistrglSerLeuProGln 75
 770 AGACTCCCACCCGGCGTGGTACCGGCACATGGCCTCCGGCGAG 819
 76 LysSerHisGlyArgThrGlnAspGluInProValValHisphePhely 92
 820 AAATCCCAAGGCCGCPACCCAGGAGAAACCCGTCGACTCTCTCAA 859
 92 SASnIleValThrProArgThrProProProserGlnGlyLysGlyArg 109
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 870 AACATITGIGACCCGGCTACCCGGCGCTCTCAGGGCAAAAGCCGTTG 919
 109 LysLeuSerLeuSerArgPheSerArgPheGlyAlaGlyIglnArgProGly 125
 920 GCCTGHCCTGAGCCTGTTAGCTGGCGCCAGGCCAGGCCAGGCCAGGCC 969
 126 PheGlyTyrGlyGlyArgAlaLeuSerAspTyrLysSerAlaHislysGly 142
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 970 TTGCGCTAGGGGCGCGTGGTCCAGTGGACTATAACTGCTCACAAAGGCT 1019
 142 eLysGlyValAspAlaGlyGlyLysLeuSerLysIlePheLysLeuGly 142
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1020 CAAGGCGTGGATGCCAGGGCACCTGTCACAAATTCAACTGGGG 1069
 159 LYATGAsPAspArgArgSerGlySerPheMetAlaIglnArg 171
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1070 GCGGTGATAGCGGTTCTGGCTCCTCGATGGCTAGCGT 1107

REGISTRATION NUMBER: 30,399
 REFERENCE/DOCKET NUMBER: ALX-129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 255 1400
 FAX: (203) 254 1101
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 131 bases
 TYPE: Nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: PCR primer Oligonucleotide 4
 HYPOTHETICAL: No
 ANTI-SENSE: Yes
 PCT-US96-0561A-8

alignment_scores:
 alignment_block:
 US-09-218-277-12 x PCT-US96-0561A-8/rev ..

Align seg 1/1 to reverse of: PCT-US96-0561A-8 from: 1 to: 131
 Quality: 236.00 Length: 43
 Ratio: 5.488 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

seq_name: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-0561A-9

seq_documentation_block:
 Sequence 9, Application PC/TUS960561A
 ; GENERAL INFORMATION:
 ; APPLICANT: Mueller, John P.
 ; APPLICANT: Lenardo, Michael J.
 ; APPLICANT: McFarland, Henry F.
 ; APPLICANT: Matis, Louis A.
 ; APPLICANT: Mueller, Eileen Elliott
 ; APPLICANT: Nye, Steven H.
 ; APPLICANT: Peifrey, Clara M.
 ; APPLICANT: Squinto, Stephen P.
 ; TITLE OF INVENTION: Modified Myelin Protein Molecules
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Maurice M. Klee
 ; STREET: 1951 Burr Street
 ; CITY: Fairfield
 ; STATE: Connecticut
 ; COUNTRY: USA
 ; ZIP: 06430

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
 COMPUTER: Macintosh Centris 610
 OPERATING SYSTEM: System 7
 SOFTWARE: Microsoft Word 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/0561A
 FILING DATE: 02-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

alignment_scores:
 alignment_block:
 US-09-218-277-12 x PCT-US96-0561A-9 ..

Align seg 1/1 to: PCT-US96-0561A-9 from: 1 to: 119
 Quality: 214.00 Length: 39
 Ratio: 5.487 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

seq_name: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-0561A-5

seq_documentation_block:
 Sequence 5, Application PC/TUS960561A
 ; GENERAL INFORMATION:
 ; APPLICANT: Mueller, John P.
 ; APPLICANT: Lenardo, Michael J.
 ; APPLICANT: McFarland, Henry F.
 ; APPLICANT: Matis, Louis A.
 ; APPLICANT: Mueller, Eileen Elliott
 ; APPLICANT: Nye, Steven H.
 ; APPLICANT: Peifrey, Clara M.
 ; APPLICANT: Squinto, Stephen P.
 ; TITLE OF INVENTION: Modified Myelin Protein Molecules
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Maurice M. Klee
 ; STREET: 1951 Burr Street
 ; CITY: Fairfield
 ; STATE: Connecticut
 ; COUNTRY: USA
 ; ZIP: 06430

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 0.8 Mb storage

COMPUTER: Macintosh Centris 610 ;
 OPERATING SYSTEM: System 7 ;
 SOFTWARE: Microsoft Word 6.0.1 ;
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US96-05611A
 FILING DATE: 02-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/431,644 ;
 FILING DATE: May 2, 1995 ;
 APPLICATION NUMBER: 08/431,648 ;
 FILING DATE: May 2, 1995 ;
 APPLICATION NUMBER: 08/482,114 ;
 FILING DATE: June 7, 1995 ;
 ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30,399
 REFERENCE/DOCKET NUMBER: ALX-129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 254 1400
 TELEFAX: (203) 254 1101
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 130 bases
 TYPE: Nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: PCR primer oligonucleotide 1
 HYPOTHEICAL: No
 ANTI-SENSE: No
 PCT-US96-05611A-5

alignment_scores:
 Quality: 188.00 Length: 35
 Percent Similarity: 100.000 Gaps: 30
 Percent Identity: 100.000

alignment_block:
 US-09-218-277-12 x PCT-US96-05611A-5 ..

Align seg 1/1 to: PCT-US96-05611A-5 from: 1 to: 130

```

  1 MetalaSerGlnlysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 17
  26 ATGGCGTCAGAACGATGCCGTCAGCGCTCAAACTCTGGC 75
  17 althAlaSerThrMetaphisAlaRArgHISlyPheLeuProArgHISa 34
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 34
  76 CACCCGCAGCACCATGGACCATGCCGTCATGCCCTCTGGCTCACC 125
  34 rgasp 35
  ||||| 130
  126 GIGAC
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seq_name: /cgnl_7/ptodata/1/ina/PCITS_COMB.seq:PCT-US96-05611A-6

GENERAL INFORMATION:
 APPLICANT: Mueller, John P.
 APPLICANT: Lenardo, Michael J.
 APPLICANT: McFarland, Henry F.
 APPLICANT: Matis, Louis A.
 APPLICANT: Mueller, Eileen Elliott
 APPLICANT: Nye, Steven H.
 APPLICANT: Pelfrey, Clara M.
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Wilkins, James A.
 TITLE OF INVENTION: Modified Myelin Protein Molecules
 NUMBER OF SEQUNCE: 29
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Maurice M. Klee ;
 STREET: 1951 Burr Street ;
 CITY: Fairfield ;
 STATE: Connecticut ;
 COUNTRY: USA ;
 ZIP: 06430 ;
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 0.8 Mb storage ;
 COMPUTER: Macintosh Centris 610 ;
 OPERATING SYSTEM: System 7 ;
 SOFTWARE: Microsoft Word 6.0.1 ;
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US96-05611A
 FILING DATE: 02-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/431,644 ;
 FILING DATE: May 2, 1995 ;
 APPLICATION NUMBER: 08/431,648 ;
 FILING DATE: May 2, 1995 ;
 APPLICATION NUMBER: 08/482,114 ;
 FILING DATE: June 7, 1995 ;
 ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30,399
 REFERENCE/DOCKET NUMBER: ALX-129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 254 1400
 TELEFAX: (203) 254 1101
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 129 bases
 TYPE: Nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: PCR primer oligonucleotide 2
 HYPOTHEICAL: No
 ANTI-SENSE: Yes
 PCT-US96-05611A-6

alignment_scores:
 Quality: 162.00 Length: 30
 Percent Similarity: 100.000 Gaps: 0
 Percent Identity: 100.000

alignment_block:
 US-09-218-277-12 x PCT-US96-05611A-6/rev ..

Align seg 1/1 to reverse of: PCT-US96-05611A-6 from: 1 to: 129

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  30 LeuproArgHISArgAspArgPheGlyIleLeuAspSerLeGlyArgPhePh 46
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 46
  128 CTGCCGCGTCACCGTGACACCGCATCTGGCTCCATCGCCGCTCTT 79
  46 eGlyGlyAspArgGlyAlaProLysArgGlySerGlyLys 59
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 59
  78 CGCGGGGAGCCGTGGCGGCCGAAGTGGCTCTGCAA 39
  seq_name: /cgnl_7/ptodata/1/ina/PCITS_COMB.seq:PCT-US96-05611A-7
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seq_documentation_block:
 ; Sequence 7, Application PC/TUS9605611A
 ; GENERAL INFORMATION:
 ; APPLICANT: Mueller, John P.
 ; APPLICANT: Lenardo, Michael J.
 ; APPLICANT: McFarland, Henry F.
 ; APPLICANT: Matis, Louis A.
 ; APPLICANT: Mueller, Eileen Elliott
 ; APPLICANT: Nye, Steven H.
 ; APPLICANT: Pelfrey, Clara M.
 ; APPLICANT: Squinto, Stephen P.

APPLICANT: Wilkins, James A.
 TITLE OF INVENTION: Modified Myelin Protein Molecules
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maurice M. Klee

STREET: 1951 Burr Street
 CITY: Fairfield
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06430

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
 OPERATING SYSTEM: System 7
 SOFTWARE: Microsoft Word 6.0.1
 APPLICATION NUMBER: PCT/US96/05611A
 FILING DATE: 02-MAY-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/431, 644
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/431, 648
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/482, 114
 FILING DATE: June 7, 1995

ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30, 399
 REFERENCE/DOCKET NUMBER: ALX-129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 255 1400
 TELEX/FAX: (203) 254 1101

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 bases
 TYPE: Nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: PCR primer oligonucleotide 3
 HYPOTHETICAL: No
 ANTI-SENSE: No
 PCT-US96-05611A-7

alignment_scores:
 Quality: 135.00 Length: 24
 Ratio: 5.625 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-218-277-12 x PCT-US96-05611A-7 ..

Align seg 1/1 to: PCT-US96-05611A-7 from: 1 to: 133

59 LysAspSerHisProAlaArgThrAlaLysGlySerLeuProGln 75
 61 AAAGACTCCACCCGGCGTACGGCAGTCCTGCGCA 110

75 DlysAspSerHisGlyArgThrGln 82
 111 GAAATCCACGGCCGTACCCAG 132

seq_name: /cgn1_7/podata/1/1na/pctus_comb.seq:PCT-US96-05611A-10
 seq_documentation_block:
 ; Sequence 10 : Application PC/TUS9605611A
 ; GENERAL INFORMATION:
 ; APPLICANT: Mueller, John P.
 ; APPLICANT: Lenardo, Michael J.
 ; APPLICANT: McFarland, Henry F.
 ; APPLICANT: Matis, Louis A.

APPLICANT: Mueller, Eileen Elliott
 APPLICANT: Nye, Steven H.
 APPLICANT: Peifrey, Clara M.
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Wilkins, James A.

TITLE OF INVENTION: Modified Myelin Protein Molecules
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maurice M. Klee

STREET: 1951 Burr Street
 CITY: Fairfield
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06430

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
 COMPUTER: Macintosh Centris 610
 OPERATING SYSTEM: System 7
 SOFTWARE: Microsoft Word 6.0.1
 APPLICATION NUMBER: PCT/US96/05611A
 FILING DATE: 02-MAY-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/431, 644
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/431, 648
 FILING DATE: May 2, 1995
 APPLICATION NUMBER: 08/482, 114
 FILING DATE: June 7, 1995

ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30, 399
 REFERENCE/DOCKET NUMBER: ALX-129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 255 1400
 TELEX/FAX: (203) 254 1101

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 111 bases
 TYPE: Nucleic acid
 STRANDEDNESS: Single
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: PCR primer oligonucleotide 6
 HYPOTHETICAL: No
 ANTI-SENSE: Yes
 PCT-US96-05611A-10

alignment_scores:
 Quality: 130.00 Length: 26
 Ratio: 5.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-218-277-12 x PCT-US96-05611A-10/rev ..

Align seg 1/1 to reverse of: PCT-US96-05611A-10 from: 1 to: 111

146 AspAlaGlyArgLysGlySerLeuProGln 162
 110 GATGCCGAGCACCTGTCATAATTCAACTGGCGCCGATAG 61

162 ArgSerGlySerPrometIlaArg 171
 60 CGGTTCTGGCTCCGATGGCTAGCT 33

Wed Sep 27 09:09:33 2000

us-09-218-277-12.rni

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OM protein - protein search, using SW model

Run on:

September 26, 2000, 19:34:34 ; Search time 12.55 seconds

(without alignments) 843.211 Million cells updates/sec

Title: US-09-218-277-12
Perfect score: 171
Sequence: 1 MASQRPSQRHGSKLATAS.....SKIFKLGGDRSRSGSPMARR 171

Scoring table: OLIGO Gapox 60.0 , Gapext 60.0

Searched: 178050 seqs, 61884766 residues

Word size : 0

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_60;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match length | DB ID | Description |
|------------|-------|--------------------|----------|-------------|
| 1 | 113 | 66.1 | 197 | 1 MBHUB |
| 2 | 76 | 44.4 | 171 | 1 NBCZB |
| 3 | 46 | 26.9 | 128 | 1 NRITS |
| 4 | 46 | 26.9 | 157 | 2 A37246 |
| 5 | 45 | 26.3 | 328 | 1 NMSB |
| 6 | 41 | 24.0 | 169 | 1 NBOB |
| 7 | 41 | 24.0 | 171 | 1 MRGB |
| 8 | 8.2 | 14 | 2 S12904 | |
| 9 | 12 | 7.0 | 42 | 2 B92087 |
| 10 | 12 | 7.0 | 174 | 2 S08535 |
| 11 | 6.4 | 33 | 2 A60222 | |
| 12 | 7 | 4.1 | 88 | 2 T43984 |
| 13 | 7 | 4.1 | 88 | 2 T44170 |
| 14 | 7 | 4.1 | 93 | 2 T09318 |
| 15 | 7 | 4.1 | 123 | 2 A69884 |
| 16 | 7 | 4.1 | 128 | 2 A60215 |
| 17 | 7 | 4.1 | 155 | 2 B32995 |
| 18 | 7 | 4.1 | 259 | 2 T17889 |
| 19 | 7 | 4.1 | 259 | 2 T29727 |
| 20 | 7 | 4.1 | 332 | 2 B70384 |
| 21 | 7 | 4.1 | 368 | 1 S64487 |
| 22 | 7 | 4.1 | 481 | 2 A60246 |
| 23 | 7 | 4.1 | 508 | 1 ND8EE3 |
| 24 | 7 | 4.1 | 529 | 2 A47131 |
| 25 | 7 | 4.1 | 532 | 2 I55389 |
| 26 | 7 | 4.1 | 532 | 2 I37188 |
| 27 | 7 | 4.1 | 545 | 2 T02279 |
| 28 | 7 | 4.1 | 545 | 2 T42593 |
| 29 | 7 | 4.1 | 573 | 2 S44605 |

ALIGNMENTS

| RESULT | 1 |
|--------|---|
| MBHUB | myelin basic protein - human |
| | Nr.Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein p |
| | 5K splice form |
| | C;Species: Homo sapiens (man) |
| | C;Date: 18-Dec-1991 #sequence_revision 25-Aug-1995 #text_change 22-Jun-1999 |
| | C;accession: S10482; A94105; B94106; A90265; JH0802; A60862; A61420; A13273; I54219; R;Streicher, R.; Stoffel, W. |
| | Biol. Chem., Hoppe-Seyler, 370, 503-510, 1989 |
| | A;Title: The organization of the human myelin basic protein gene. Comparison with the |
| | A;Reference number: S10482; MUID:89302693 |
| | A;accession: S10482 |
| | A;Status: translation not shown |
| | A;Molecule type: DNA |
| | A;Residues: 1-197 <STR> |
| | A;Cross-references: EMBL:X17286; MIG:934490; PIDN:CAA35179.1; PID:e221974; PID:g11842 |
| | R;Kamholz, J.; De Ferrer, F.; Puchett, C.; Lazzarini, R. |
| | Proc. Natl. Acad. Sci. U.S.A., 86, 4982-4986, 1989 |
| | A;Title: Identification of three forms of human myelin basic protein by cDNA cloning. |
| | A;Reference number: A94106; MUID:8629714 |
| | A;accession: A94106 |
| | A;Molecule type: mRNA |
| | A;Residues: 1-59; 86-197 <KAN> |
| | A;Cross-references: GB:MI3577; PID:9187408; PIDN:AAA59562.1; PID:g307150 |
| | A;Note: 18.5K splice form |
| | A;accession: B94106 |
| | A;Molecule type: mRNA |
| | A;Residues: 1-197 <KA2> |
| | A;Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form |
| | A;Note: a 17.2K splice form is also described |
| | A;Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form; a 17.2K |
| | R;Carnehl, P.R. |
| | Biochem. J., 123, 57-67, 1971 |
| | A;Title: Amino acid sequence of the encephalitogenic basic protein from human myelin. |
| | A;Reference number: A90256; MUID:72066400 |
| | A;accession: A90256 |
| | A;Molecule type: protein |
| | A;Residues: 2-59; 86-197 <CAR> |
| | R;Proost, P.; Van Damme, J.; Odenakker, G. |
| | Biochem. Biophys. Res. Commun., 192, 1175-1181, 1993 |
| | A;Title: Leukocyte gelatinase B cleavage releases encephalitogens from human myelin b |
| | A;Reference number: JH0802; MUID:93282820 |
| | A;accession: JH0802 |
| | A;Molecule type: protein |
| | A;Residues: 2-59; 86-197 <PRO> |
| | A;Experimental source: brain |
| | R;Scoble, H.A.; Whitaker, J.N.; Blennemann, K. |
| | J. Neurochem., 47, 614-616, 1986 |
| | A;Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44 |
| | A;Reference number: A60862; MUID:86280476 |
| | A;accession: A60862 |

A: Molecule type: protein
A: Residues: 2-45;117-197 <SCo>
A: Note: evidence for acetylated amino end
R. Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Blemann, K.
J. Biol. Chem. 259: 5028-5031, 1984
A: Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined by
A: Reference number: A61420; NUID:84185508
A: Accession: A61420
A: Molecule type: protein
A: Residues: 46-59; 86-116 <GIB>
R. Wood, D.D.; Moscarello, M.A.
J. Biol. Chem. 254: 5121-5127, 1989
A: Title: The isolation, characterization, and lipid-aggregating properties of a citrulline-rich peptide from human myelin basic protein
A: Reference number: A33273; NUID:89174797
A: Accession: A33273
A: Molecule type: protein
A: Residues: 15-25; 'X', 27-31, 'X', 33-59; 86-148, 'X', 150-156, 'X', 158-185, 'X', 187-196, 'X' <WCO>
A: Note: form C-8; residues designated 'X' were determined as citrulline
R. Baldwin, G.S.; Carnegie, P.R.
Biochem. J. 123: 69-74, 1971
A: Title: Isolation and partial characterization of methylated arginines from the encephalomyelitis virus
A: Reference number: A90557; NUID:7206601
A: Contents: annotation
A: Note: Arg-134 may be unmethylated, monomethylarginine, or dimethylarginine in the approx.
R. Lennon, V.A.; Wiks, A.V.; Carnegie, P.R.
J. Immunol. 105: 1223-1230, 1971
A: Reference number: A92806; NUID:71088405
A: Contents: annotation
A: Note: a region including residues 139-149 induces experimental autoimmune encephalomyelitis in mice
R. Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.E.; Prusiner, S.B.
Genomics 6, 16-22, 1990
A: Title: Repetitive DNA (TGG)n^{5'} to the human myelin basic protein gene: a new form of repetitive DNA
A: Reference number: I54219; NUID:90152079
A: Accession: I54219
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-59 <RES>
A: Cross-references: GB:M63590; NID:918402; PIDN:AAA55560..1; PID:918403
R. Roth, H.J.; Kronquist, K.E.; Keleiro de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.
J. Neurosci. Res. 17, 321-326, 1987
A: Title: Evidence for the expression of four myelin basic protein variants in the developing mouse brain
A: Reference number: I56567; NUID:87311781
A: Accession: I56567
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: mRNA
A: Residues: 1-132;144-197 <RT2>
A: Cross-references: GB:M30516; NID:9187410; PIDN:AAA59563..1; PID:9307161
A: Accession: I17634
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: mRNA
A: Residues: 1-197 <RE3>
A: Cross-references: GB:M30515; NID:9187412; PIDN:AAA59564..1; PID:9307162
R. Roth, H.J.; Kronquist, K.; Pretorius, P.J.; Crandall, B.F.; Campagnoni, A.T.
J. Neurosci. Res. 16, 227-239, 1986
A: Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin basic protein
A: Reference number: I56565; NUID:86308101
A: Accession: I56565
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: mRNA
A: Residues: 1-159 <RE4>
A: Cross-references: GB:M30047; NID:9187400; PIDN:AAA59559..1; PID:9307159
R. Arch. Biochem. Biophys. 322: 174-182, 1995
A: Title: The isolation and characterization of four myelin basic proteins from the unbroken rat sciatic nerve
A: Reference number: S66383; NUID:9604793
A: Accession: S66383
A: Molecule type: protein
A: Residues: 23-25; 'X', 27-39 <BOU>
C: Comment: Four alternatively spliced forms of myelin basic protein have been observed,
C: Genetics:
A: Gene: GDB:MEP
A: Map position: 18q22-18qter

Qy 2 ASQKRPSPQRHSKYLATASTMDHARHGFLPPLRHDGILDSIGRFF 47
 Db 1 ASQKRPSPQRHSKYLATASTMDHARHGFLPPLRHDGILDSIGRFF 46

RESULT 5

MBNSB
 goll-myelin basic protein precursor - mouse
 N;Alternate names: goll-mbp protein; MBP
 N;Contains: myelin basic protein

C;Species: Mus musculus (house mouse)
 C;Date: 17-Mar-1987 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
 C;Accession: A4521; B4542; A0875; A9067; A26591; B26591; A60920; I48407; I5996;
 R;Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Land
 J. Biol. Chem. 268, 4930-4938, 1993
 A;Title: Structure and developmental regulation of Goll-mbp, a 105-kilobase gene tha

A;Reference number: A45421; MUID:93186801

A;Accession: A45421

A;Molecule type: mRNA

A;Residues: 46-86 <MCF>

A;Note: the sequence reported for this encephalitogenic peptide differs from that shown

R;Roach, A.; Boylan, K.; Horvath, S.; Prusiner, S.B.; Hood, L.E.
 Cell 34, 799-806, 1983

A;Title: Characterization of cloned cDNA representing rat myelin basic protein: absence

A;Reference number: A21062; MUID:84026484

A;Accession: A21062

A;Molecule type: mRNA

A;Residues: 1-124; T, 126-128 <ROA>

A;Experimental source: strain Sprague-Dawley

C;Keywords: alternative splicing; blocked amino end; experimental autoimmune encephalomy

F;2-128;Product: myelin basic protein S #statac experimental <MAT>
 F;2/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #statu
 F;105/Modified site: omega-N-methylarginine or omega-N,omega-N-dimethylarginine (Arg) (

Query Match 26.9%; Score 46; DB 1; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.7e-41; P-value 0;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASQKRPSPQRHSKYLATASTMDHARHGFLPPLRHDGILDSIGRFF 46
 Db 1 MASQKRPSPQRHSKYLATASTMDHARHGFLPPLRHDGILDSIGRFF 46

RESULT 4

A;Accession: A37246

A;Molecule type: protein

N;Alternate names: myelin AI protein

C;Species: Cavia porcellus (guinea pig)

C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 07-Oct-1994

C;Accession: A37246; C92087; A03440

R;Deibel, G.E.; Martensen, R.E.; Krutzsch, H.C.; Kies, M.W.
 J. Neurochem. 43, 100-105, 1984

A;Title: Sequence of guinea pig myelin basic protein.

A;Reference number: A37246; MUID:84215086

A;Accession: A37246

A;Molecule type: protein

A;Status: preliminary

A;Residues: 1-167 <DER>

R;Shapiro, R.; McNealy, S.S.; Chou, F.; Kibler, R.F.
 J. Biol. Chem. 246, 4630-4640, 1971

A;Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin

A;Reference number: A92087

A;Accession: C92087

A;Molecule type: protein

A;Residues: 45-87 <SHA>

C;Superfamily: myelin basic protein

C;Keywords: myelin

Query Match 26.9%; Score 46; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 3.4e-41; P-value 0;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQKRPSPQRHSKYLATASTMDHARHGFLPPLRHDGILDSIGRFF 47
 Db 1 ASQKRPSPQRHSKYLATASTMDHARHGFLPPLRHDGILDSIGRFF 46

RESULT 5

MBNSB
 goll-myelin basic protein precursor - mouse
 N;Alternate names: goll-mbp protein; MBP
 N;Contains: myelin basic protein

C;Species: Mus musculus (house mouse)
 C;Date: 17-Mar-1987 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
 C;Accession: A4521; B4542; A0875; A9067; A26591; B26591; A60920; I48407; I5996;
 R;Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Land
 J. Biol. Chem. 268, 4930-4938, 1993
 A;Title: Structure and developmental regulation of Goll-mbp, a 105-kilobase gene tha

A;Reference number: A45421; MUID:93186801

A;Accession: A45421

A;Molecule type: mRNA

A;Residues: 1-190; 217-276; 316-328 <CAM1>

A;Note: sequence extracted from NCBI backbone (NCBIN:126696) and modified

A;Accession: B45421

A;Status: preliminary

A;Molecule type: mRNA

A;Accession: 1-191; 'SSEP' <CAM2>

A;Cross-references: GB:L075058; NID:gi193586; PIDN:AAA37721.1; PID:gi193587

A;Experimental source: clone B21

A;Note: sequence extracted from NCBI backbone (NCBIN:126700; NCBIPI:126715)
 Rde Ferrar, F.; Eng, H.; Hudson, L.; Kahlholz, J.; Puckett, C.; Molineaux, S.; Lazzar
 Cell 43, 721-727, 1985

A;Title: Alternative splicing accounts for the four forms of myelin basic protein.

A;Reference number: A90875; MUID:86079555

A;Accession: A90875

A;Molecule type: mRNA

A;Residues: 134-328 <DEF>

A;Cross-references: GB:L00404; GB:ML1669; NID:gi199060; PIDN:AAA39502.1; PID:g387419

A;Experimental source: 21.5K

R;Takahashi, N.; Roach, A.; Teplow, D.B.; Prusiner, S.B.; Hood, L.
 Cell 42, 139-148, 1985

A;Title: Cloning and characterization of the myelin basic protein gene from mouse: on

A;Reference number: A90867; MUID:85254913

A;Accession: A90867

A;Molecule type: DNA

A;Residues: 134-190; 217-328 <TKR>

A;Cross-references: GB:ML1533; NID:gi199044; PIDN:AAA39496.1; PID:g387414

A;Experimental source: 18.5K

R;Newman, S.; Kitamura, K.; Campagnoni, A.T.;
 Proc. Natl. Acad. Sci. U.S.A. 84, 866-890, 1987

A;Title: Identification of a cDNA coding for a fifth form of myelin basic protein in

A;Reference number: A94188; MUID:87118269

A;Accession: A94188

A;Molecule type: DNA

A;Residues: 134-274; 316-328 <NEW1>

A;Cross-references: GB:ML050; NID:gi199048; PIDN:AAA59711.1; PID:gi199049

A;Experimental source: clone M22; Splice form 17-22K

A;Accession: B26591

A;Molecule type: mRNA

A;Residues: 134-190; 217-263; 275-328 <NEW2>

A;Cross-references: GB:ML062; NID:gi199050

A;Experimental source: clone M28; splice form 17-24K

R;Kitamura, K.; Newman, S.L.; Campagnoni, C.W.; Verdi, J.M.; Mohandas, T.; Handley, V.
 J. Neurochem. 54, 2033-2041, 1990

A;Title: Expression of a novel transcript of the myelin basic protein gene.

A;Reference number: A60920

A;Accession: A60920

A;Molecule type: mRNA

A;Residues: 134-190; 217-224; 316-328 <KIT>

A;Status: translation not shown

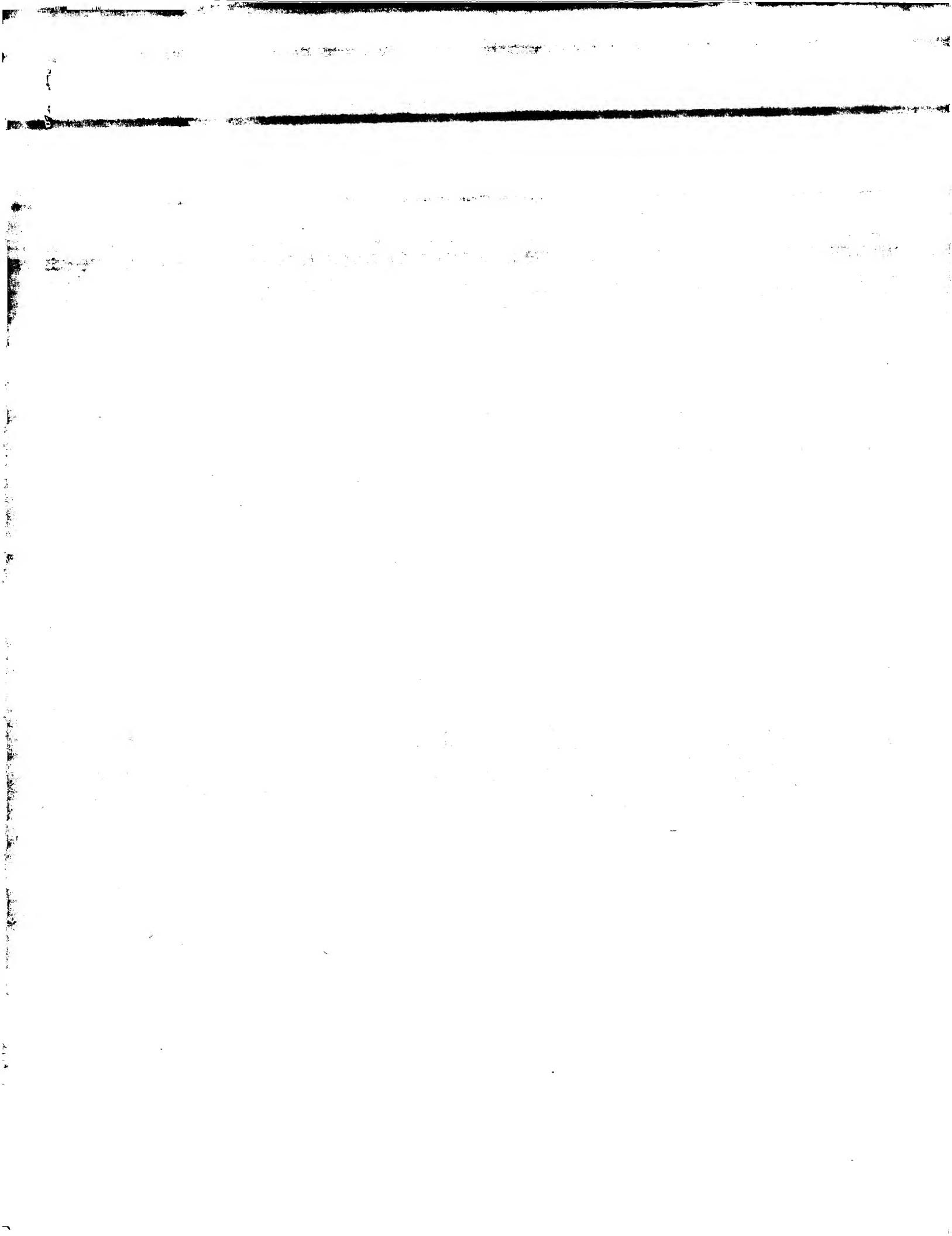
A;Experimental source: M41; splice form 14K

| | |
|---|--|
| Ri-Grima, B.; Zelenka, D.; Pessac, B. | A; Title: Basic AI protein of the myelin membrane. The complete amino acid sequence. |
| J. Neurochem. 59, 2316-2323, 1992 | A; Reference number: A92089; MUID:72007306 |
| A; Reference number: I48407; MUID:93057537 | A; Accession: A92089 |
| A; Status: preliminary; translated from GB/EMBL/DDJB | A; Molecule type: Protein |
| A; Residues: 1-191; SSEP' <GLI> | A; Residues: 1,'S,2-169 <EYL> |
| A; Cross-references: EMBL:X67319; NID:951332; PIDN:CAA47733.1; PID:951333 | R; Brostoff, S.W.; Reuter, W.; Hichens, M.; EYlar, E.H. |
| A; Note: submitted to the EMBL Data Library, July 1992 | J. Biol. Chem. 249, 559-567, 1974 |
| A; Reference number: I48407; MUID:93057537 | A; Title: Specific cleavage of the AI protein from myelin with cathepsin D. |
| A; Accession: I48407 | A; Reference number: A92160; MUID:74070588 |
| A; Status: preliminary; translated from GB/EMBL/DDJB | A; Molecule type: protein |
| A; Molecule type: mRNA | A; Residues: 1-169 <BRO> |
| A; Residues: 219-248 <ELI> | R; Shapia, R.; McNeally, S.S.; Chou, F.; Kibler, R.F. |
| A; Accession: I58996; MUID:84119431 | J. Biol. Chem. 246, 4330-4340, 1971 |
| A; Status: preliminary; translated from GB/EMBL/DDJB | A; Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine myelin basic protein. |
| A; Molecule type: mRNA | A; Reference number: A92087 |
| A; Residues: 219-248 <ELI> | A; Accession: A92087 |
| A; Accession: I58996; MUID:84119431 | A; Molecule type: protein |
| A; Status: preliminary; translated from GB/EMBL/DDJB | A; Residues: 43-87 <SHA> |
| A; Molecule type: DNA | R; Okazaki, K.; Oopata, N.H.; Inoue, S.; Hidaka, H. |
| A; Residues: 134-157 <MIU> | Biochem. J. 306, 551-555, 1995 |
| A; Cross-references: GB:M24410; NID:9199052; PIDN:AAA39498.1; PID:9554195 | A; Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in g |
| A; Reference number: I54033; MUID:89252919 | Neurochem. Res. 17, 239-246, 1992 |
| A; Accession: I54033 | A; Reference number: S54343; MUID:95194333 |
| A; Status: preliminary; translated from GB/EMBL/DDJB | A; Molecule type: protein |
| A; Molecule type: DNA | A; Residues: 74-75; HG,78-82; D,84-88; 105, X,107-108, X,110-114, X,116-119 <OKA> |
| A; Residues: 31-38, 1989 | R; Takamatsu, K.; Tatenumo, K. |
| A; Cross-references: GB:M36775; NID:9199059; PIDN:AAA39504.1; PID:9293725 | Neurochem. Res. 17, 239-246, 1992 |
| A; Reference number: I54033; MUID:89252919 | A; Title: Isolation and characterization of two novel peptide amides originating from |
| A; Title: Gene organization and transcription of duplicated MBP genes of myelin deficient rat. Reference number: I53236; MUID:88196094 | A; Reference number: A61641; MUID:92319189 |
| A; Accession: I53236 | A; Molecule type: protein |
| A; Status: translation not shown; translated from GB/EMBL/DDJB | A; Residues: 1-12 <TAK> |
| A; Molecule type: DNA | A; Accession: B61641 |
| A; Residues: 217-229, 'HN', 232-250 <OKA> | A; Molecule type: protein |
| A; Cross-references: GB:M36775; NID:9199059; PIDN:AAA39504.1; PID:9293725 | A; Residues: 1-16 <TA2> |
| A; Reference number: I54033; MUID:89252919 | A; Note: these peptides have carboxyl-terminal amides probably produced by a non-enzymatic process. |
| A; Note: hypothetical translation of the reversed and complementary sequence to that shown above. Reference number: I54033; MUID:89252919 | R; Brostoff, S.; Elyar, E.H. |
| A; Note: mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.24K, 17.22K and 17.20K | Proc. Natl. Acad. Sci. U.S.A. 68, 765-769, 1971 |
| A; Note: myelin basic protein (MBP) is a major component of myelin. It is composed of five different forms of the protein: 21.5K, 18.5K, 17.24K, 17.22K and 17.20K. The 21.5K form is the most abundant. The 18.5K form is the second most abundant. The 17.24K form is the third most abundant. The 17.22K form is the fourth most abundant. The 17.20K form is the fifth most abundant. | A; Title: Localization of methylated arginine in the AI protein from myelin. |
| A; Gene: Goli-1-mbp; sh1-mld | A; Reference number: A93777; MUID:71153946 |
| A; Introns: 190/3; 250/3; 262/3; 273/3; 314/3 | A; Contents: annotation |
| C; Function: | A; Note: Arg-106 is modified to monomethylarginine and dimethylarginine |
| A; Description: probably helps maintain myelin structure | R; Syiar, E.H.; Caccam, J.J.; Jackson, J.J.; Westfall, F.C.; Robinson, A.B. |
| C; Superfamily: myelin basic protein | A; Title: Experimental allergic encephalomyelitis: synthesis of disease-inducing site |
| C; Keywords: alternative splicing; myelin; structural protein | A; Reference number: A94241; MUID:70178977 |
| F1-190, 217-276, 316-328/Product: myelin basic protein, splice form 21.5K #status predicted <MAT> | A; Contents: annotation |
| F134-328/Product: myelin basic protein, splice form 17K-a #status predicted <MAT> | A; Note: the region including residues 114-122 induces experimental allergic encephalomyelitis. |
| F1-134-374, 316-328/Product: myelin basic protein, splice form 18.5K #status predicted <MAT> | C; Superfamily: myelin basic protein |
| F134-190, 217-263, 316-328/Product: myelin basic protein, splice form 18.5K #status predicted <MAT> | C; Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephalomyelitis. |
| F134-190, 217-263, 316-328/Product: myelin basic protein, splice form 14K #status predicted <MAT> | F1-169/Product: myelin basic protein #status experimental <MAT> |
| F1-134-190, 217-274, 316-328/Product: myelin basic protein, splice form 14K #status predicted <MAT> | F1-169/Product: myelin peptide amide-16 #status experimental <PA16> |
| Query Match | F1-12/Modified site: myelin peptide amide-12 #status experimental <PA12> |
| Best Local Similarity | F1-1/Modified site: acetylated amino end (Ala) #status experimental <PA1> |
| Matches | F1-2/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide amide-12) |
| 45; Conservative | F1-16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide amide-16) |
| 0; Mismatches | F1-106/Modified site: omega-N-methylarginine or omega-N-dimethylarginine (Arg) |
| 0; Indels | RESULT 6 |
| 0; Gaps | Query Match |
| 0; 0; | Best Local Similarity |
| 0; 0; | Matches |
| 0; 0; | Conservative |
| 0; 0; | Mismatches |
| 0; 0; | Indels |
| 0; 0; | Gaps |
| 0; 0; | MBQB |
| N; Myelin basic protein - bovine | Query Match |
| N; Alternative names: myelin AI protein | Best Local Similarity |
| N; Contains: myelin peptide amide-12 (MPA-12); myelin peptide amide-16 (MPA-16) | Matches |
| C; Species: Bos primigenius taurus (cattle) | 100.0%; Score: 41; DB 1; length: 169; |
| C; Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 07-May-1999 | Pred. No. 7.2e-36; Pred. 0; Mismatches 0; |
| C; Accession: A92089; A92160; A92087; S55433; A51641; B65641; A03140 | Indels 0; Gaps 0; |
| R; Eylar, E.H.; Brostoff, S.; Hashim, G.; Caccam, J.; Burnett, P. | RESULT 7 |
| J. Biol. Chem. 246, 5770-5784, 1971 | Query Match |
| Db 234 HRTQDENPVVHFKNIVTPRTPPSOGKGRGLSLSRFWGEGQ 278 | Best Local Similarity |
| Db 78 HQTQDENPVVHFKNIVTPRTPPSOGKGRGLSLSRFWGEGQ 122 | 100.0%; Score: 41; DB 1; length: 169; |
| Db 234 HRTQDENPVVHFKNIVTPRTPPSOGKGRGLSLSRFWGEGQ 278 | Pred. No. 7.2e-36; Pred. 0; Mismatches 0; |
| Db 78 HQTQDENPVVHFKNIVTPRTPPSOGKGRGLSLSRFWGEGQ 122 | Indels 0; Gaps 0; |
| Db 80 QDENPVVHFKNIVTPRTPPSOGKGRGLSLSRFWGEGQ 120 | Indels 0; Gaps 0; |
| N; Myelin basic protein - pig (tentative sequence) | RESULT 7 |
| N; Alternative names: myelin AI protein | Query Match |
| N; Contain: myelin basic protein | Best Local Similarity |
| N; Alternative names: myelin AI protein | Matches |
| N; Contain: myelin basic protein | Conservative |
| N; Alternative names: myelin AI protein | Mismatches |
| N; Contain: myelin basic protein | Indels |
| N; Alternative names: myelin AI protein | Gaps |
| N; Contain: myelin basic protein | MBQB |

| | |
|---|--|
| N;Contains: myelin basic protein amide 14 | J. Biol. Chem. 246, 4630-4640, 1971 |
| C;Species: Sus scrofa domesticus (domestic pig) | A;Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine brain peptide 1-171. |
| C;Date: 19-Apr-1996 #text_change 07-May-1999 | A;Reference number: A92087 |
| C;Accession: A61640; A36245 | A;Accession: B92087 |
| R;Kira, J.; Delbier, G.E.; Krutsch, H.C.; Martenson, R.E. | A;Molecule type: Protein |
| J; Neurochem. 44, 134-142, 1985 | A;Residues: 1-14 <SMA> |
| A;Title: Amino acid sequence of porcine myelin basic protein. | C;Superfamily: Myelin basic protein |
| A;Reference number: A61640; MUID:85056964 | C;Keywords: myelin |
| A;Accession: A61640 | |
| A;Molecule type: protein | |
| A;Residues: 1-14 <TAK> | |
| A;Note: this sequence in the abstract is inconsistent with that in figure 3 in having Glu C;Superfamily: myelin basic protein | |
| C;Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephalomyelitis (EAE) model | |
| F;1-171/Product: myelin basic protein #status experimental <PAT> | |
| F;1-14/Modified site: acetylated amino end (Ala) #status experimental <PA12> | |
| F;14/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide amide 1-14) | |
| F;107/Modified site: omega-N-methylarginine or omega-N',omega-N'-dimethylarginine (Arg) (amide in mature form myelin peptide amide 1-107) | |
| Query Match | Best Local Similarity 7.0%; Score 12; DB 2; Length 42; |
| Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY 82 QDENPVYHFKIYVTPPPSQQCKRGSLSRFSRGAEGQ 122 | QY 49 DRGAKPKGSKD 60 |
| Db 81 QDENPVYHFKIYVTPPPSQQCKRGSLSRFSRGAEGQ 121 | Db 4 DRGAKPKGSKD 15 |
| RESULT 8 | RESULT 10 |
| S12904 protein kinase (EC 2.7.1.37) - starfish (<i>Pisaster ochraceus</i>) | S08535 myelin basic protein - chicken |
| C;Species: Pisaster ochraceus | C;Species: Gallus gallus (chicken) |
| C;Accession: S12904 | C;Accession: S08535 |
| R;BS Jett. 27, 223-226, 1990 | R;Zopf, D.; Sonntag, V.; Betz, H.; Gundelfinger, E.D. |
| A;Title: Identification of the sites in myelin basic protein that are phosphorylated by protein kinase C - starfish | Glia, 2, 241-249, 1989 |
| A;Reference number: S12904; MUID:91032186 | A;Title: Developmental accumulation and heterogeneity of myelin basic protein transcr |
| A;Accession: S12904 | A;Reference number: S08535; MUID:89358239 |
| A;Status: preliminary | A;Accession: S08535 |
| A;Molecule type: protein | A;Molecule type: mRNA |
| A;Residues: 1-14 <SAN> | A;Residues: 1-174 <ZOP> |
| C;Keywords: phosphotransferase | A;Cross-references: EMBL:X17103; NID:963594; PID:CAA34959.1; PID:963595 |
| RESULT 9 | Query Match |
| B92087 Query Match | Best Local Similarity 100.0%; Score 12; DB 2; Length 42; |
| Best Local Similarity 100.0%; Score 14; DB 2; Length 14; | Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | QY 148 QGTLSKFKLGG 159 |
| Db 1 NIVTPRTPPSQCK 106 | Db 147 QGTRSKFKLGG 158 |
| RESULT 11 | Query Match |
| A60222 Query Match | Best Local Similarity 100.0%; Score 12; DB 2; Length 42; |
| myelin basic protein - mouse (fragment) | Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| C;Species: Mus musculus (house mouse) | QY 107 GRLSRSFW 117 |
| C;Accession: A60222 | Db 23 GRLSRSFW 33 |
| R;Aruga, J.; Okano, H.; Mikoshiba, K. | |
| J. Neurochem. 56, 1222-1226, 1991 | |
| A;Title: Identification of the new isoforms of mouse myelin basic protein: the existence of two distinct forms of the protein | |
| A;Reference number: A60222; MUID:91162193 | |
| A;Accession: A60222 | |
| A;Status: preliminary | |
| A;Molecule type: mRNA | |
| A;Residues: 1-33 <ARU> | |
| RESULT 9 | Query Match |
| B92087 Query Match | Best Local Similarity 100.0%; Score 11; DB 2; Length 33; |
| Best Local Similarity 100.0%; Score 14; DB 2; Length 14; | Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | QY 107 GRLSRSFW 117 |
| Db 1 NIVTPRTPPSQCK 14 | Db 23 GRLSRSFW 33 |
| RESULT 12 | Query Match |
| Ta3984 Query Match | Best Local Similarity 100.0%; Score 11; DB 2; Length 33; |
| Best Local Similarity 100.0%; Score 14; DB 2; Length 14; | Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | QY 107 GRLSRSFW 117 |
| Db 23 GRLSRSFW 33 | |
| C;Species: Oryctolagus cuniculus (domestic rabbit) | |
| C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 30-Sep-1993 | |
| C;Accession: B92087; A03140 | |
| R;Shapiro, R.; McNeilly, S. S.; Chou, P.; Kihler, P. | |

Wed Sep 27 09:09:34 2000

us-09-218-277-12.rpr



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OM protein - protein search, using sw model

Run on: September 26, 2000, 19:36:23 ; Search time 7.44 Seconds.

(without alignments)
112.250 Million cell updates/sec

Title: US-09-218-277-12

Perfect score: 171

Sequence: 1 MASQKRPSQRHGSKYLATAS.....SKIEFLGGDRSRSGSPMARR 171

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 85661 seqs, 30989116 residues

Word size : 0

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Swissprot_38;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

1 113 66.1 196 1 NBP_HUMAN
P05686 homo sapien
P05686 canis troglodytes
P21188 cavia porcellus
P05688 rattus norvegicus
P04370 mus musculus
P05687 bos taurus
P81558 sus scrofa
P25274 oryctolagus cuniculus
P17720 gallus gallus
Q91325 raja erinaceus
Q91439 squalus acanthias
P80083 amphidinium
P20939 heterodontus
P52995 saccharomyces cerevisiae
Q63313 rattus norvegicus
P20919 equus caballus
P43007 homo sapiens
P34280 caenorhabditis elegans
P52347 herpes simplex virus type 1
Q25190 manduca sexta
P80232 locusta migratoria
P81198 stylochaetina
Q60885 mus musculus
P24020 sus scrofa
P40542 saccharomyces cerevisiae
P30985 synchococcus sp
Q08044 bovine heart
P30660 pseudorabies virus
P77162 escherichia coli
P11339 zea mays (millet)
P05424 oryza sativa
P0545 oryctolagus cuniculus
P16290 escherichia coli

Searched: 85661 seqs, 30989116 residues

Word size : 0

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Swissprot_38;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

1 186 1 TRIS_HUMAN
P19237 homo sapiens
P13413 rattus norvegicus
Q53805 mus musculus
O74110 thermoplasmatales
P9950 pseudomonas
Q8055 methanococcus
P47200 pseudomonas
Q31458 bacillus subtilis
Q10426 schizosaccharomyces pombe
Q12574 schizosaccharomyces pombe
Q10153 schizosaccharomyces pombe
P17514 nicotiana tabacum

ALIGNMENTS

RESULT 1

| ID | MBP_HUMAN | STANDARD; | PRT; | 196 AA. |
|----|---|-----------|------|---------|
| AC | P02686; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 01-NOV-1991 (Rel. 20, Last sequence update) | | | |
| DT | 15-FEB-2000 (Rel. 39, Last annotation update) | | | |
| DE | MYELIN BASIC PROTEIN (MBP). | | | |
| GN | MBP, | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo. | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE: 89302693. | | | |
| RA | Streicher R., Stoffel W., | | | |
| RT | "The organization of the human myelin basic protein gene. Comparison with the mouse gene.", | | | |
| RL | Biol. Chem. Hoppe-Seyler 370:503-510(1989). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE: 87311781. | | | |
| RA | Roth H.J., Kronquist K.E., de Rosbo N., Crandall B.F., | | | |
| RA | Campagnoni A.T., | | | |
| RT | "Evidence for the expression of four myelin basic protein variants in the developing human spinal cord through cDNA cloning.", | | | |
| RL | J. Neurosci. Res. 17:321-328(1987). | | | |
| RN | [3] | | | |
| RT | SEQUENCE OF 1-58; 85-131 AND 143-196 FROM N.A. | | | |
| RP | MEDLINE: 86508101. | | | |
| RA | Roth H.J., Kronquist K.E., Pretorius P.J., Crandall B.F., | | | |
| RA | Campagnoni A.T., | | | |
| RT | "Isolation and characterization of a cDNA coding for a novel human herpes basic protein (MBP) variant.", | | | |
| RL | J. Neurosci. Res. 17:227-238(1986). | | | |
| RN | [4] | | | |
| RP | SEQUENCE OF 1-58 AND 85-196 FROM N.A. | | | |
| RX | MEDLINE: 86259714. | | | |
| RA | Kamholz J., de Ferrer F., Puckett C., Lazzarini R.A., | | | |
| RT | "Identification of three forms of human myelin basic protein by cDNA cloning.", | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986). | | | |
| RN | [5] | | | |
| RP | SEQUENCE OF 1-58 AND 85-196. | | | |
| RX | MEDLINE: 72056400. | | | |
| RA | Carnegie P.R., | | | |
| RT | "Amino acid sequence of the encephalitogenic basic protein from human myelin.", | | | |
| RL | Biochem. J. 123:57-67(1971). | | | |
| RN | [6] | | | |
| RP | SEQUENCE OF 45-58 AND 85-114, AND REVISIONS. | | | |
| RA | Shepria R., McKneally S.S., Chou F., Kibler R.P., | | | |
| RT | "Encephalitogenic fragment of myelin basic Protein. Amino acid sequence of bovine, rabbit, guinea pig, monkey, and human fragments.", | | | |
| RL | J. Biol. Chem. 246:4650-4640(1971). | | | |
| RN | [7] | | | |

RP SEQUENCE OF 1-58 FROM N.A.
 RX MEDLINE: 90152679.
 RA Boylan K.B., Ayres T.M., Popko B., Takahashi N., Hood L.E.,
 RA Prusiner S.B.;
 RT "Repetitive DNA (TGG)_n 5' to the human myelin basic protein gene: a
 new form of Oligonucleotide repetitive sequence showing length,
 RT polymorphism";
 RT Genomics 6:16-22(1990).
 [8]
 RP METHYLATION.
 RX MEDLINE: 72066401.
 RA Baldwin G.S., Carnegie P.R.;
 RT Isolation and partial characterization of methylated arginines from
 the encephalitogenic basic protein of myelin;";
 RL Bichem. J 123:69-74(1971).
 CC -!- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -!- ALTERNATIVE PRODUCTS: THREE ISOMERS; 21.5 kDa (SHOWN HERE), 18.5
 KDa (THE MOST ABUNDANT) AND 17.2 kDa; ARE PRODUCED BY ALTERNATIVE
 CC SPlicing.
 CC -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC
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 CC
 CC PRELIMINARYSEQUENCE.
 CC MEDLINE: 76005821.
 RA Westall F.C., Thompson M., Kalter S.S.;
 RT "The Proposed sequence of the encephalitogenic protein from
 OC Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 [1]
 RN DE MBP_BASIC_PROTEIN (MBP).
 RN DE MBP.
 RN DE pan_troglodytes (Chimpanzee).
 RN DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 RN DE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 RN DE MBP.
 RN DE Life Sci. 17:219-223(1975).
 CC -!- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC MEDLINE: 76005821.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 DR PIR: A03139; MBCZB.
 DR PFAM: PF0069; Myelin_MBP; 1.
 DR PRINS; PRO0212; MYELIN_NMBP.
 DR PROSITE; PS0059; MYELIN_MBP; 1.
 DR EMBL; X17287; CAA35179.1; JOINED.
 DR EMBL; M13577; AAA59562.1; -.
 DR EMBL; M30516; AAA59563.1; -.
 DR EMBL; M30515; AAA59564.1; -.
 DR EMBL; M30047; AAA59559.1; -.
 DR EMBL; X17286; CAA35179.1; -.
 DR EMBL; X17287; CAA35179.1; JOINED.
 DR EMBL; M13577; AAA59562.1; JOINED.
 DR EMBL; X17288; CAA35179.1; JOINED.
 DR EMBL; X17289; CAA35179.1; JOINED.
 DR EMBL; X17290; CAA35179.1; JOINED.
 DR PIR; S10482; S10482.
 DR PIR: 159430; -.
 DR PFAM: PF0069; Myelin_MBP; 1.
 DR PRINS; PRO0212; MYELIN_NMBP.
 DR PROSITE; PS0059; MYELIN_MBP; 1.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis; Alternative splicing.
 FT INIT_MET 0 0 ACETYLATION.
 FT MOD_RES 1 1 METHYLATION (MONO-:6% OR DI-:60%).
 FT DOMAIN 133 133 INDUCES EXPERIMENTAL AUTOIMMUNE
 FT MOD_RES 45 114 ENCEPHALOMYELITIS IN MONKEYS, RABBITS,
 FT DOMAIN 138 148 AND RATS BUT NOT IN GUINEA PIGS.
 FT VARSPLIC 59 84 INDUCES EXPERIMENTAL AUTOIMMUNE
 FT MISSING (IN 18.5 kDa ISOFORM AND 17.2 kDa
 FT ISOFORM).
 FT VARSPLIC 132 142 MISSING (IN 17.2 kDa ISOFORM).
 SQ SEQUENCE 196 AA; 21362 MW; 23EBDOC1C689653 CRC64;

Query Match Score 44.4%; Score 76; DB 1; Length 171;
 Best Local Similarity 100.0%; Pred. No. 1.8e-72; Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQKPSQRGSKVLTASTMDHARRHGFPLPRHDTGILDSIGRFGGDRGAPRGSGKDS 61
 Db 1 ASQKPSQRGSKVLTASTMDHARRHGFPLPRHDTGILDSIGRFGGDRGAPRGSGKDS 60

OY 62 HHPARTAHGSPRS 77
 Db 61 HHPARTAHGSPRS 76

RESULT 3
 NMBP_CAVPO STANDARD; PRT: 167 AA.
 ID NMBP_CAVPO
 AC P25188;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 OS Cavia porcellus (Guinea Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 84215086.
 RA Deibler G.E., Martenson R.E., Krutzsch H.C., Kies M.W.,
 RT "Sequence of guinea pig myelin basic protein.";
 RL J. Neurochem. 43:100-105(1984).
 RN [2]
 SEQUENCE OF 45-87.
 RA Shapira R., McKeaneally S.S., Chou F., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";

Query Match Score 113; DB 1; Length 196;
 Best Local Similarity 100.0%; Pred. No. 2.5e-111; Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KDSHPARTAHGSPRSQKSHRTQPENPVHFKVNTPRPPPSQKKGGLSLSRFSWQ 118
 Db 84 KDSHPARTAHGSPRSQKSHRTQPENPVHFKVNTPRPPPSQKKGGLSLSRFSWQ 143

OY 119 AEGQPGFGIGGRASDIKSAHKGFKGVDAQTLSKIFKLGRDSRSGSPMARR 171

RL J. Biol. Chem. 246:4630-4640(1971).
 CC -!- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 DR PIR: A37245; A37246.
 DR PIR; C92087; C22087.
 DR PFAM: PF01669; MYELIN-MBP; 1.
 DR PRINTS: PRO0212; MYELIN-MBP.
 DR PROSITE; PS0569; MYELIN-MBP; 1.
 KW Myelin; structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis.
 MOD_RBS 1 ACETYLATION.
 MOD_RBS 1 METHYLATION (MONO- OR DI-) (BY
 FT 106 106 SIMILARITY).
 FT DOMAIN 114 122 INDUCES EXPERIMENTAL AUTOIMMUNE
 FT SEQUENCE 167 AA; 18213 MW; 88D31F1B5ACFAA6 CRC64;
 RESULT 4
 MBP_RAT ID MBP_RAT STANDARD; PRT; 127 AA.
 AC P02698;
 DT 21-JUL-1996 (Rel. 01, Created)
 DT 21-JUL-1996 (Rel. 01, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN S (MBP S).
 GN MBP.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Rattus.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE; 8702649.
 RA Schach M., Budzinski R.M., Stoffel W.;
 RT "Cloned proteolipid protein and myelin basic protein cDNA.
 RT Transcription of the two genes during myelination.";
 RL BIOL. Chem. Hoppe-Seyler 357:825-834(1986).
 RN [2] SEQUENCE FROM N.A.
 RP MEDLINE; 84026484.
 RA Roach A., Boylan K., Horvath S., Prusiner S.B., Hood L.E.;
 RT "Characterization of cloned cDNA representing rat myelin basic
 protein: absence of expression in brain of shiverer mutant mice.",
 RT Cell 34:799-806(1983).
 RN [3] SEQUENCE.
 RP MEDLINE; 75127359.
 RA Dunkley P.R., Carnegie P.R.;
 RT "Amino acid sequence of the smaller basic protein from rat brain
 myelin.",
 RL Biochem. J. 141:243-255(1974).
 RP SEQUENCE OF 45-85.
 RX MEDLINE; 73180720.
 RA McFarlin D.E., Blank S.E., Khler R.F., McKneally S., Shapira R.;
 RT "Experimental allergic encephalomyelitis in the rat: response to
 RT encephalitogenic proteins and peptides.",
 RL Science 179:478-480(1973).
 CC -!- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -!- ALTERNATIVE PRODUCTS: RATS HAVE TWO MYELIN BASIC PROTEINS. THE

CC SMALLER ONE, SHOWN HERE, IS MISSING 40 RESIDUES (FOLLOWING RESIDUE
 CC 113 OR 114) WITH RESPECT TO THE LARGER ONES FROM OTHER SPECIES.
 CC -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC
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 DR EMBL_M25889; AAA1575_1; -.
 DR EMBL_K00512; -, NOT_ANNOTATED_CDS.
 DR PIR; A03142; MERTS.
 DR PIR; B24351; B24351.
 DR PIR; A21062; A21062.
 DR PFAM: PF01669; Myelin-MBP; 1.
 DR PRINTS; PRO0212; MYELIN-MBP.
 KW Myelin; structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis; Alternative splicing.
 FT INIT-MET 0 0
 MOD_RBS 1 ACETYLATION.
 MOD_RBS 104 104 METHYLATION (MONO-44% OR DI-11%).
 FT CONFFLICT 46 47 SG -> GS (IN REF. 4).
 FT CONFFLICT 124 124 M -> I (IN REF. 2).
 SQ SEQUENCE 127 AA; 14080 MW; B4C9F33C19A8E137_CRC64;

RESULT 5
 MBP_MOUSE ID MBP_MOUSE STANDARD; PRT; 194 AA.
 AC P04310;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-AN-1988 (Rel. 06, last sequence update)
 DT 01-OCT-1996 (Rel. 34, last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 GN MBP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN SEQUENCE FROM N.A. (ALL FOUR FORMS).
 RP MEDLINE; 86019555.
 RA de Ferra F., Engh H., Hudson L., Kamholz J., Puckett C., Molineaux S.,
 RA Lazzarini R.A.;
 RT "Alternative splicing accounts for the four forms of myelin basic
 RT protein.",
 RL Cell 43:721-727(1985).
 RN [2] SEQUENCE FROM N.A. (18.5 KDA FORM).
 RP MEDLINE; 85254913.
 RA Takahashi N., Roach A., Teplow D.B., Prusiner S.B., Hood L.;
 RT "Cloning and characterization of the myelin basic protein gene from
 mouse: One gene can encode both 14 kd and 18.5 kd MBPs by alternate
 RT use of exons.",
 RL Cell 42:139-148(1985).
 RN [3] SEQUENCE FROM N.A. (17 KDA FORM).
 RP MEDLINE; 87118269.
 RA Newman S., Kiamura K., Campagnoni A.T.;
 RT "Identification of a cDNA coding for a fifth form of myelin basic
 protein in mouse.",

| | | | | |
|----|---|-----------|---|---|
| RL | PROC. NATL. ACAD. SCI. U.S.A. 84:886-890(1987). | PT | | ISOFORM); MISSING (IN 17 kDa ISOFORM AND 14 kDa |
| RN | [4] | PT | VARSPLIC | 140 180 |
| RP | SEQUENCE OF 1-23 FROM N.A. | FT | | MISSING (IN 17 kDa ISOFORM). |
| RX | MEDLINE; 89352919. | FT | SEQUENCE | 194 AA; 21371 MW; D20BAC0CF52ACD2 CRC64; |
| RA | Mura M., Tamura T.A., Aoyama A., Mikoshiba K.; | SO | | |
| RT | "the promoter elements of the mouse myelin basic protein gene function efficiently in NG108-15 neuronal/glial cells.", | OT | 78 HGRTDENPVHFFNIVPPRTPPSQGIGRGLSLSFSGWAGCQ | 122 |
| RT | Gene 75:31-38(1999). | DR | 100 HGRTDENPVHFFNIVPPRTPPSQGIGRGLSLSFSGWAGCQ | 144 |
| CC | - - FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE | Db | | |
| CC | - - OF MYELIN. | | | |
| CC | - - SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN. | | | |
| CC | - - SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY. | | | |
| CC | - - ALTERNATIVE PRODUCTS: FOUR ISOFORMS; 21.5 kDa (SHOWN HERE), 18.5 kDa, 17 kDa AND 14 kDa; ARE PRODUCED BY ALTERNATIVE SPLICING. | | | |
| CC | - - - SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY. | | | |
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| CC | ----- | | | |
| DR | EMLB; M11533; AAA39495_1; . | RESULT | 6 | |
| DR | EMLB; M11291; AAA39496_1; JOINED. | MPB_BOVIN | | |
| DR | EMLB; M11529; AAA39496_1; JOINED. | STANDARD; | | |
| DR | EMLB; M11530; AAA39495_1; JOINED. | PRT; | 169 AA. | |
| DR | EMLB; M11531; AAA39496_1; JOINED. | AC | | |
| DR | EMLB; M11532; AAA39496_1; JOINED. | DT | 21-JUL-1986 (Rel. 01, Created) | |
| DR | EMLB; M11533; AAA39497_1; JOINED. | DT | 21-JUL-1986 (Rel. 01, Last sequence update) | |
| DR | EMLB; M11291; AAA39497_1; JOINED. | DT | 15-FEB-2000 (Rel. 39, Last annotation update) | |
| DR | EMLB; M11529; AAA39497_1; JOINED. | DE | MYELIN BASIC PROTEIN (MPB) (MYELIN AI PROTEIN). | |
| DR | EMLB; M11530; AAA39497_1; JOINED. | GN | MPB. | |
| DR | EMLB; M11531; AAA39497_1; JOINED. | OS | Bos taurus (Bovine). | |
| DR | EMLB; M11532; AAA39497_1; JOINED. | OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| DR | EMLB; M11533; AAA39497_1; JOINED. | OC | Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; | |
| DR | EMLB; M11291; AAA39497_1; JOINED. | OC | Bovinae; Bovinae; Bos. | |
| DR | EMLB; M11529; AAA39497_1; JOINED. | RN | [1] | |
| DR | EMLB; M11530; AAA39497_1; JOINED. | REVISION. | | |
| DR | EMLB; M11531; AAA39497_1; JOINED. | RP | SEQUENCE. | |
| DR | EMLB; M11532; AAA39497_1; JOINED. | RP | MEMLINE; 72007306. | |
| DR | EMLB; M11533; AAA39497_1; JOINED. | RX | EYLAR E.H., BROSTOFF S.W., HASHIM G., CACCAM J., BURNETT P.; | |
| DR | EMLB; L00398; AAA39500_1; . | RA | "Basic AI protein of the myelin membrane. The complete amino acid | |
| DR | EMLB; L00399; AAA39500_1; JOINED. | RT | sequence.", | |
| DR | EMLB; L00400; AAA39500_1; JOINED. | RL | J. Biol. Chem. 246:5770-5784(1971). | |
| DR | EMLB; L00401; AAA39500_1; JOINED. | RN | [2] | |
| DR | EMLB; L00402; AAA39500_1; JOINED. | REVISION. | | |
| DR | EMLB; L00403; AAA39500_1; JOINED. | RP | MEMLINE; 74070588. | |
| DR | EMLB; L00404; AAA39500_1; . | RA | BROSTOFF S.W., REUTER W., RICHENS M., EYLAR E.H.; Hashim G., Caccam J., Burnett P.; | |
| DR | EMLB; L00398; AAA39500_1; JOINED. | RT | "Specific cleavage of the AI protein from myelin with cathepsin D.", | |
| DR | EMLB; L00399; AAA39500_1; JOINED. | RL | J. Biol. Chem. 249:559-567(1974). | |
| DR | EMLB; L00401; AAA39501_1; JOINED. | RN | [3] | |
| DR | EMLB; L00402; AAA39501_1; JOINED. | REVISION. | | |
| DR | EMLB; L00403; AAA39501_1; JOINED. | RP | SEQUENCE OF 43-87. | |
| DR | EMLB; L00404; AAA39501_1; . | RA | SHAPIRA R., MCNEALLY S.S., CHOU F., KIBLER R.F.; | |
| DR | EMLB; L00398; AAA39502_1; JOINED. | RT | "Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine, rabbit, guinea pig, monkey, and human fragments.", | |
| DR | EMLB; L00399; AAA39502_1; JOINED. | RL | J. Biol. Chem. 246:4630-4640(1971). | |
| DR | EMLB; L00401; AAA39502_1; JOINED. | RN | [4] | |
| DR | EMLB; L00402; AAA39502_1; JOINED. | REVISION. | | |
| DR | EMLB; L00403; AAA39502_1; JOINED. | RP | METHYLATION. | |
| DR | EMLB; L00404; AAA39502_1; JOINED. | RX | MEMLINE; 71153946. | |
| DR | EMLB; L00398; AAA39502_1; JOINED. | RA | BROSTOFF S.W., EYLAR E.H.; Localization of methylated arginine in the AI protein from myelin.", | |
| DR | EMLB; L00399; AAA39502_1; JOINED. | RT | Proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971). | |
| DR | EMLB; L00401; AAA39502_1; JOINED. | RL | SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION. | |
| DR | EMLB; L00402; AAA39502_1; JOINED. | RN | MEMLINE; 70178977. | |
| DR | EMLB; L0003; AAA39502_1; JOINED. | RA | EYLAR E.H., CACCAM J., JACKSON J.J., WESTALL F.C., ROBINSON A.B.; | |
| DR | EMLB; M15060; AAA59711_1; . | RT | "Experimental allergic encephalomyelitis: synthesis of disease-inducing site of the basic protein.", | |
| DR | EMLB; M24410; AAA39498_1; . | RL | Science 168:1220-1223(1970). | |
| DR | EMLB; A24772; MBMB. | CC | I - FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE | |
| DR | PIR; A26591; A26591. | CC | OF MYELIN. | |
| DR | PIR; B26591; B26591. | CC | - - SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN. | |
| DR | MCD; MGI:96925; MBP. | CC | - - SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY. | |
| DR | PEPAB; PF01669; Myelin-MBP; 1. | CC | PIR; A03140; MBBOB. | |
| DR | PRINTS; PR00212; MYELIN-MBP. | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| DR | PROSITE; PS00569; MYELIN-MBP; 1. | CC | PRINTS; PR00212; MYELIN-MBP. | |
| KW | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| KW | Autoimmune encephalomyelitis; Alternative splicing. | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | INIT_MET 0 | CC | Autoimmune encephalomyelitis. | |
| FT | MOD_RES 1 1 | CC | PIR; A03140; MBBOB. | |
| FT | MOD_RES 130 130 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | VARSPLIC 57 82 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PFAM; PF01669; Myelin-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PRINTS; PR00212; MYELIN-MBP. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PROSITE; PS00569; MYELIN-MBP; 1. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | Autoimmune encephalomyelitis. | |
| FT | MISSING (IN 18.5 kDa ISOFORM AND 14 kDa DOMAIN 114 122 | CC | PIR; A03140; MBBOB. | |
| | | | | |

FT
SQ SEQUENCE 169 AA; 18323 MW; ENCEPHALOMYELITIS.
 Best Local Similarity 24.0%; Score 41; DB 1; Length 169;
 Matches 41; Conservative 100.0%; Pred. No. 1e-35; 0; Mismatches 0;
 DE Myelin BASIC PROTEIN (MBP).
 DB 80 QDENPVVHFFKNTIVPRTPPSQGKGRLSLSRSGAEGQ 122
 DE MYELIN BASIC PROTEIN (MBP).
 GN MBP.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-BRAIN;
 RX MEDLINE: 85055964.
 RA Ira J.-I., Deibler G.E., Krutschach H.C., Martenson R.E.;
 RT "Amino acid sequence of porcine myelin basic protein."
 RL J. Neurochem. 44:134-142(1985).
 CC !- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 OF MYELIN.
 CC !- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC !- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 DR PROSTTE; PS0069; MYELIN MBP; 1.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 Autoimmune encephalomyelitis.
 FT MOD_RES 1 107 ACETYLATION.
 FT DOMAIN 115 123 METHYLATION (MONO- OR DI-) (BY
 FT INDUCES EXPERIMENTAL AUTOIMMUNE
 FT ENCEPHALOMYELITIS (BY SIMILARITY).
 SQ SEQUENCE 171 AA; 18487 MW; 287AEDF2F24028D9 CRC64;

RESULT 7
 MBP_PIG STANDARD; PRT; 171 AA.
 ID MBP_PIG
 AC P81558;
 DT 15-FEB-2000 (Rel. 39, Created)
 DT 15-FEB-2000 (Rel. 39, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 MBP.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-BRAIN;
 RX MEDLINE: 85055964.
 RA Ira J.-I., Deibler G.E., Krutschach H.C., Martenson R.E.;
 RT "Amino acid sequence of porcine myelin basic protein."
 RL J. Neurochem. 44:134-142(1985).
 CC !- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 OF MYELIN.
 CC !- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC !- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 DR PROSTTE; PS0069; MYELIN MBP; 1.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 Autoimmune encephalomyelitis.
 FT MOD_RES 1 107 ACETYLATION.
 FT DOMAIN 115 123 METHYLATION (MONO- OR DI-) (BY
 FT INDUCES EXPERIMENTAL AUTOIMMUNE
 FT ENCEPHALOMYELITIS (BY SIMILARITY).
 SQ SEQUENCE 171 AA; 18487 MW; 287AEDF2F24028D9 CRC64;

Query Match 24.0%; Score 41; DB 1; Length 171;
 Best Local Similarity 100.0%; Score 12; DB 1; Length 169;
 Matches 41; Conservative 100.0%; Pred. No. 1e-35; 0; Mismatches 0;
 DE Myelin BASIC PROTEIN (MBP).
 DB 81 QDENPVVHFFKNTIVPRTPPSQGKGRLSLSRSGAEGQ 122
 DE MYELIN BASIC PROTEIN (MBP).
 GN MBP.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 SEQUENCE.
 RA Shapira, R.; McKneally S.S.; Chou, F.; Kibler, R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments."
 RESULT 8
 MBP_RABBIT STANDARD; PRT; 42 AA.
 ID MBP_RABBIT
 AC P25274;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP) (MYELIN AI PROTEIN) (FRAGMENT).
 GN MBP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 SEQUENCE.
 RA Shapira, R.; McKneally S.S.; Chou, F.; Kibler, R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments."
 RESULT 9
 MBP_CHICK STANDARD; PRT; 173 AA.
 ID MBP_CHICK
 AC P15720;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WHITE LEghORN; TISSUE-BRAIN;
 RX MEDLINE; 8935239.
 RA Zopf D., Sonnag H., Gundelfinger E.D.;
 RT "Developmental accumulation and heterogeneity of myelin basic protein
 transcripts in the chick visual system.";
 RL Glia 2:241-249(1989).
 CC !- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 OF MYELIN.
 CC !- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC !- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 DR EMBL: X17103; CAA39595.;
 DR PIR; S08335; S08353.
 DR PFAM: PF01669; Myelin MBP; 1.
 DR PRINTS; PR0021; MYELINMBP.
 DR PROSTTE; PS0069; MYELIN MBP; 1.
 DR Myelin; Structural protein; Acetylation; Methylation; Phosphorylation.
 FT INT-MET 0 0
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT MOD_RES 105 105 105 METHYLATION (BY SIMILARITY).
 SQ SEQUENCE 173 AA; 1867 MW; AB2770DAC9CF019D CRC64;

Query Match 7.0%; Score 12; DB 1; Length 173;
 Best Local Similarity 100.0%; Score 12; DB 1; Length 173;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Heiling U.; Hofmann B.; Delius H.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE GPI-OBG FAMILY.

RESULT 13
 MBD_HETFR STANDARD; PRT; 154 AA.
 ID MBD_HETTR
 AC P0939;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 GN MBP.
 OS Heterodontus francisci (Horn shark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Heterodontidae; Heterodontidae;
 OC Heterodontiformes; Heterodontidae; Heterodontidae.
 RN [1]
 RP TISSUE=BRAIN;
 RC
 RX MEDLINE; 90040744.
 RA Saavedra R.A., Fors L., Aebersold R.H., Arden B., Horvath S.,
 RA Sanders J., Hood L.;
 RT The myelin proteins of the shark brain are similar to the myelin
 proteins of the mammalian peripheral nervous system.;
 RL J. Mol. Evol. 29:149-156(1999).
 CC -!- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 OF MYELIN.
 CC -!- SUBCELLULAR LOCATION: CYTOSPLASMIC SIDE OF MYELIN.
 CC -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.

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 between the European Bioinformatics Institute and the EMBL outstation -
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 or send an email to license@isb-sib.ch).

CC DR EMBL; 272958; CAQ97199; 1.
 DR PRFM; PR01018; GPL1_OBG; 1.
 DR PRINS; PR0326; GPILOBG.
 KW Hypothetical Protein; GTP-binding.
 FT NP_BIND 70 77 GTP (BY SIMILARITY).
 FT NP_BIND 116 120 GTP (BY SIMILARITY).
 FT NE_BIND 250 253 GTP (BY SIMILARITY).
 SQ SEQUENCE 368 AA; 41006 MW; D144569C9C5D777C CRC64;

CC DR EMBL; X17664; CAA35661; 1; -.
 DR PIR; B32999; B32999.
 DR PFAM; PRO166; Myelin_MBP; 1.
 DR PROSITE; PS00569; MYELIN_MBP; 1.
 DR INIT_MET 0 BY SIMILARITY.
 DR MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 DR SEQUENCE 154 AA; 16502 MW; A9A57DA149429A83 CRC64;

Query Match 4.1%; Score 7; DB 1; Length 368;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC RN RESULT 15
 ID LBP_RAT STANDARD; PRT; 481 AA.
 AC Q96313;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP).
 GN LBP.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
 RX MEDLINE; 94222804.
 RA Su G.L.; Freewick P.D.; Geller D.A.; Wang O.; Shapiro R.A.; Wan Y.H.;
 RA Billiar T.R.; Twardy D.J.; Simmons R.L.; Wang S.C.;
 RA "Molecular cloning, characterization, and tissue distribution of rat
 RT RT lipopolysaccharide binding protein. Evidence for extrahepatic
 RT RT expression." 153:743-752(1994).
 RL J. Immunol.
 CC -!- FUNCTION: BINDS TO THE LIPID A MOIETY OF BACTERIAL
 CC LIPOPOLYSACCHARIDES (LPS), A GLICOOLIPID PRESENT IN THE OUTER
 CC MEMBRANE OF ALL GRAM-NEGATIVE BACTERIA. THE LBP/LPS COMPLEX SEEMS
 CC TO INTERACT WITH THE CD14 RECEPTOR.
 CC -!- SIMILARITY: BELONGS TO THE BPI/CCEP/LBP/PLP FAMILY.

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 or send an email to license@isb-sib.ch).

CC DR EMBL; I32132; AAA01835; 1; -.
 DR HSSP; P17213; 1BP2.

DR PFAM; PF0273; LBP_BPL_CEMP; 1.
DR PROSITE; PS00400; LBP_BPL_CEP; 1.
KW LIPID transport; Antibiotic; transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 481 LIPOPOLYSACCHARIDE-BINDING PROTEIN.
FT CARBONID 300 300 POTENTIAL.
FT CARBONID 355 355 POTENTIAL.
SQ SEQUENCE 481 AA; 53600 MW; 23E67CB9CC97D2FC CRC64;

Query Match 4.1%; Score 7; DB 1; Length 481;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 GRGLSLS 113
||| |||||
Db 98 GRGLSLS 104

Search completed: September 26, 2000, 19:38:14
Job time: 111 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2000, 19:36:43 ; Search time 13.52 Seconds

(without alignments)
876.933 Million cell updates/sec

Title: US-09-218-277-12

Perfect score: 171

Sequence: 1 MASQKRPSQRHGSKYLATAS.....SKIFKLGGGRDSRSGPMMR 171

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 225878 seqs, 69334122 residues

Word size : 0

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SPREMBL_12;*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mmc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match length | DB ID | Description |
|------------|-------|--------------------|-------|-------------|
| 1 | 171 | 100.0 | 304 | 4 Q15340 |
| 2 | 59 | 34.5 | 197 | 4 Q15339 |
| 3 | 46 | 26.9 | 1154 | 11 Q921J5 |
| 4 | 46 | 26.9 | 169 | 11 Q921J5 |
| 5 | 46 | 26.9 | 195 | 11 Q921J4 |
| 6 | 34 | 19.9 | 149 | 11 Q91835 |
| 7 | 34 | 19.9 | 195 | 11 Q011585 |
| 8 | 34 | 19.9 | 250 | 11 Q03139 |
| 9 | 17 | 9.9 | 34 | 11 Q61837 |
| 10 | 8 | 4.7 | 176 | 13 P87346 |
| 11 | 8 | 4.7 | 281 | 10 Q38690 |
| 12 | 7 | 4.1 | 87 | 12 Q9559 |
| 13 | 7 | 4.1 | 88 | 12 Q9WT40 |
| 14 | 7 | 4.1 | 93 | 12 Q69048 |
| 15 | 7 | 4.1 | 123 | 2 Q31793 |
| 16 | 7 | 4.1 | 140 | 10 Q9XFE2 |
| 17 | 7 | 4.1 | 259 | 5 Q21174 |
| 18 | 7 | 4.1 | 259 | 12 Q98438 |
| 19 | 7 | 4.1 | 332 | 2 Q67104 |

ALIGMENTS

| RESULT | 1 | ID | PRELIMINARY; | PRT; | 304 AA. |
|-----------------------|---|--------|--------------|------|---------|
| Q15340 | | Q15340 | | | |
| AC | Q15340; | | | | |
| DT | 01-NOV-1996 (REMBLrel. 01, Created) | | | | |
| DT | 01-NOV-1996 (REMBLrel. 01, Last sequence update) | | | | |
| DT | 01-NOV-1999 (REMBLrel. 12, Last annotation update) | | | | |
| DE | GOLI-MBP. | | | | |
| OS | Homo sapiens (Human), | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; | | | | |
| OC | Buteraria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| RN | {1} | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE-BRAIN; | | | | |
| RA | MEDLINE; 94068468. | | | | |
| RA | PRIBL T.M., CAMPAGNONI C.W., KAMPF K., KASHIMA T., HANDLEY V.W., | | | | |
| RA | MCMAON J., CAMPAGNONI A.T.; | | | | |
| RT | "The human myelin basic protein gene is included within a 179-kilobase transcription unit: expression in the immune and central nervous systems." | | | | |
| RT | systems."; | | | | |
| RT | Proc. Natl. Acad. Sci. U.S.A. 90:10695-10699(1993). | | | | |
| DR | EMBL; L18866; AAA72011.1; | | | | |
| DR | PROSITE; PS00569; MYELIN-MBP. 1. | | | | |
| DR | SEQUENCE; PR00212; MYELIN-MBP. | | | | |
| DR | SEQUENCE 304 AA; 3317 MW; 4E9B0AE CRC32; | | | | |
| Query Match | 100 %; Score 171; DB 4; Length 304; | | | | |
| Best Local Similarity | 100.0%; Score 171; DB 4; Length 304; | | | | |
| Matches | 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
| Qy | 1 MASQKRPSQRHGSKYLATAS...TMDHARHGFTPRHRDTGILSIGRPGFGDRGAPRKGSKD 60 | | | | |
| Db | 134 MASQKRPSQRHGSKYLATAS...TMDHARHGFTPRHRDTGILSIGRPGFGDRGAPRKGSKD 193 | | | | |
| Qy | 61 SHHPARTARYGLPSKPSKHTQDENDPVWPHFKNTWPRTPPPSQGKGKGSLSRPSWGA 120 | | | | |
| Db | 194 SHHPARTAHYGLSPKPSKHTQDENDPVWPHFKNTWPRTPPPSQGKGKGSLSRPSWGA 253 | | | | |
| Qy | 121 GQRPGFGYSRASDYSKAHKGKQYDAQTLISKFLKGDRRSRGSPMARR 171 | | | | |
| Db | 254 GQRPGFGYSRASDYSKAHKGKQYDAQTLISKFLKGDRRSRGSPMARR 304 | | | | |

| | | | | |
|--|--|--|-----------------------|---|
| | | | DT | 01-NOV-1999 (TREMBlrel. 12, Last annotation update) |
| | | | DE | MELIN BASIC PROTEIN. |
| | | | GN | MBP. |
| | | | OS | Rattus norvegicus (rat). |
| | | | OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; |
| | | | RN | Bacteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. |
| | | | RP | [1] SEQUENCE FROM N.A. |
| | | | RC | STRAIN=LEWIS RAT; |
| | | | RA | LOBELL A.M.; WIGZELL H.; |
| | | | RL | Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases. |
| | | | DR | EMBL; AJ135897; CAAL0806_1; -. |
| | | | DR | PROSITE; PS00569; MYELIN_MBP; 1. |
| | | | SQ | SEQUENCE 169 AA; 18470 MW; BOA7CCAO CRC32; |
| | | | | |
| | | | RESULT | 2 |
| | | | Query Match | 34.5%; Score 59; DB 4; Length 197; |
| | | | Best Local Similarity | 100.0%; Pred. No. 2.8e-55; |
| | | | Matches | 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| | | | ID | Q921J6 |
| | | | AC | Q921J6; |
| | | | PRELIMINARY; | PRT; 154 AA. |
| | | | DT | 01-MAY-1999 (TREMBlrel. 10, Created) |
| | | | DT | 01-MAY-1999 (TREMBlrel. 10, Last sequence update) |
| | | | Db | 134 MASQKPSQRHSKYLATASTMHDHARGFLPRHRDTGILDSSIGRFF 46 |
| | | | | MASQKPSQRHSKYLATASTMHDHARGFLPRHRDTGILDSSIGRFF 46 |
| | | | | MELIN BASIC PROTEIN. |
| | | | | Rattus norvegicus (Rat). |
| | | | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; |
| | | | | Bacteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. |
| | | | | [1] SEQUENCE FROM N.A. |
| | | | | STRAIN=LEWIS RAT; |
| | | | | LOBELL A.M.; WIGZELL H.; |
| | | | | Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases. |
| | | | | EMBL; AJ135898; CAAL0807_1; -. |
| | | | | PROSITE; PS00569; MYELIN_MBP; 1. |
| | | | | SEQUENCE 195 AA; 21484 MW; 79E5D9D CRC32; |
| | | | | |
| | | | RESULT | 3 |
| | | | Query Match | 26.9%; Score 46; DB 11; Length 195; |
| | | | Best Local Similarity | 100.0%; Pred. No. 2.3e-41; |
| | | | Matches | 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| | | | ID | Q921J6 |
| | | | AC | Q921J6; |
| | | | PRELIMINARY; | PRT; 154 AA. |
| | | | DT | 01-MAY-1999 (TREMBlrel. 10, Last sequence update) |
| | | | DT | 01-MAY-1999 (TREMBlrel. 12, Last annotation update) |
| | | | Db | 134 MASQKPSQRHSKYLATASTMHDHARGFLPRHRDTGILDSSIGRFF 46 |
| | | | | MASQKPSQRHSKYLATASTMHDHARGFLPRHRDTGILDSSIGRFF 46 |
| | | | | MELIN BASIC PROTEIN. |
| | | | | Rattus norvegicus (Rat). |
| | | | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; |
| | | | | Bacteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. |
| | | | | [1] SEQUENCE FROM N.A. |
| | | | | STRAIN=LEWIS RAT; |
| | | | | LOBELL A.M.; WIGZELL H.; |
| | | | | Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases. |
| | | | | EMBL; AJ135898; CAAL0807_1; -. |
| | | | | PROSITE; PS00569; MYELIN_MBP; 1. |
| | | | | SEQUENCE 154 AA; 17207 MW; F3971OB CRC32; |
| | | | | |
| | | | RESULT | 4 |
| | | | Query Match | 26.9%; Score 46; DB 11; Length 154; |
| | | | Best Local Similarity | 100.0%; Pred. No. 1.9e-41; |
| | | | Matches | 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| | | | ID | Q921J5 |
| | | | AC | Q921J5; |
| | | | PRELIMINARY; | PRT; 169 AA. |
| | | | DT | 01-MAY-1999 (TREMBlrel. 10, Created) |
| | | | DT | 01-MAY-1999 (TREMBlrel. 10, Last sequence update) |
| | | | Db | 1 MASQKPSQRHSKYLATASTMHDHARGFLPRHRDTGILDSSIGRFF 46 |
| | | | | MASQKPSQRHSKYLATASTMHDHARGFLPRHRDTGILDSSIGRFF 46 |
| | | | | MELIN BASIC PROTEIN (FRAGMENT). |
| | | | | Mus musculus (Mouse). |
| | | | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; |
| | | | | Bacteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| | | | | [1] SEQUENCE FROM N.A. |
| | | | | STRAIN=C57BL/6J; TISSUE-BRAIN; |
| | | | | MEDLINE: 87118259. |
| | | | | NEWMAN S., KITAMURA K., CAMPAGNONI A.T.; |
| | | | | "Identification of a cDNA coding for a fifth form of myelin basic |
| | | | | protein." |

| | | | | |
|----------|---|---|---|----------------------------|
| RT | protein in mouse." | DT | 01-NOV-1996 (TREMBLrel. 01, last sequence update) | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 84:886-890(1987). | DE | MYELIN BASIC PROTEIN (MBP). | |
| DR | EMBL: M1062; ARB:9712.1; -. | OS | Mus musculus (Mouse). | |
| PROSITE: | PS00569; MYELIN-MBP; 1. | OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; | |
| KW | Alternative splicing; Myelin. | OC | Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus. | |
| FT | NON-TER 1 | RN | [1] | |
| SQ | SEQUENCE 149 AA; 16226 MW; A6DC1599 CRC32; | RQ | SEQUENCE FROM N.A. | |
| RESULT | 7 | RC | STRAIN=C7BL/6; TISSUE=BRAIN; | |
| Q01585 | PRELIMINARY; PRT; 195 AA. | RX | CAMPAGNONI A.T., PRIBYL T.M., CAMPAGNONI C.W., KAMPF K., GARBY B., AMURUMARKEE S., LANDRY C., HANDLEY V., NEWMAN S., GARBY B., KITAMURA K.; MEDLINE: 93106801. | |
| ID | Q01585 | RA | "Structure and developmental regulation of Goll-1-mbp, a 105-kilobase gene that encompasses the myelin basic protein gene and is expressed in cells in the oligodendrocyte lineage in the brain." | |
| AC | Q01585; | RT | J. Biol. Chem. 268:4930-4933(1993). | |
| DT | 01-NOV-1996 (TREMBLrel. 01, last sequence update) | DR | EMBL: L01507; AAA37720.1; -. | |
| DE | MYELIN BASIC PROTEIN (MBP). | PRINS; PR00212; MYELIN-MBP. | | |
| GN | NBp. | KW | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; Autoimmune encephalomyelitis; Alternative splicing. | |
| OS | Mus musculus (Mouse). | SQ | SEQUENCE 250 AA; 27167 MW; 3A08ADE7 CRC32; | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; | Db | 144 SKYLATASMDHARRHGFPLPRHRTGILDLSIGRF 46 | |
| RN | Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus. | Qy | 13 SKYLATASMDHARRHGFPLPRHRTGILDLSIGRF 46 | |
| RP | SEQUENCE FROM N.A. | DT | 01-NOV-1996 (TREMBLrel. 01, last sequence update) | |
| RC | STRAIN=C7BL/6; TISSUE=BRAIN; | DE | 01-NOV-1996 (TREMBLrel. 12, last annotation update) | |
| RX | STRAIN=C57 BLACK; TISSUE=BONE MARROW; | GN | MYELIN BASIC PROTEIN (FRAGMENT). | |
| RA | GRIMA B., ZELENKA D., PESSAC B.: | RA | SHI-MLD. | |
| RT | "A novel transcript overlapping the myelin basic protein gene." | OS | Mus musculus (Mouse). | |
| RL | J. Neurochem. 59:2318-2323(1992). | OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; | |
| RN | [2] | OC | Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus. | |
| RP | SEQUENCE FROM N.A. | RN | [1] | |
| RT | CAMPAGNONI A.T., PRIBYL T.M., CAMPAGNONI C.W., KAMPF K., GARBY B., AMURUMARKEE S., LANDRY C., HANDLEY V., NEWMAN S., GARBY B., KITAMURA K.; | RP | SEQUENCE FROM N.A. | |
| RT | "Structure and developmental regulation of Goll-1-mbp, a 105-kilobase gene that encompasses the myelin basic protein gene and is expressed in cells in the oligodendrocyte lineage in the brain." | RA | MEDLINE: 93106801. | |
| RT | J. Biol. Chem. 268:4930-4933(1993). FUNCTION TO MAINTAIN PROPER STRUCTURE OF MYELIN. | RA | MEDLINE: 88106094. | |
| CC | -!- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN. | RA | KIKUCHIBA K.; MEDLINE: X67319; CAA47733.1; -. | |
| CC | EMBL: X67319; CAA47733.1; -. | RT | "Gene organization and transcription of duplicated MBP genes of myelin deficient (shi/mld) mutant mouse." | |
| DR | EMBL: L07508; AAA37721.1; -. | RT | EMBO J. 7:77-83(1988). | |
| DR | MGB; MGI:96925; Mbp. | RL | DR | EMBL: M3675; AAA3504.1; -. |
| KW | Myelin; Structural protein; Acetylation; Methylation; Phosphorylation; Autoimmune encephalomyelitis; Alternative splicing. | PROSITE; PS00569; MYELIN-MBP; 1. | | |
| SQ | SEQUENCE 195 AA; 21004 MW; 55D83EA CRC32; | KW | Myelin. | |
| RESULT | 9 | FT | NON-TER 1 1 | |
| Q061037 | PRELIMINARY; PRT; 34 AA. | FT | NON-TER 34 34 | |
| ID | Q061037 | SQ | SEQUENCE 34 AA; 3958 MW; 31F53967 CRC32; | |
| AC | Q061037 | Qy | Query Match 9.9%; Score 17; DB 11; Length 34; | |
| DT | 061037; 1996 (TREMBLrel. 01, last sequence update) | Best Local Similarity 100.0%; Pred. No. 6e-11; Length 34; | | |
| Matches | 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | Matches | 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Qy | 13 SKYLATASMDHARRHGFPLPRHRTGILDLSIGRF 46 | Qy | 78 HGRTQDENPVWHEFKNI 94 | |
| Db | 144 SKYLATASMDHARRHGFPLPRHRTGILDLSIGRF 177 | Db | 18 HGRTQDENPVWHEFKNI 34 | |
| RESULT | 8 | RESULT | 10 | |
| Q03139 | PRELIMINARY; PRT; 250 AA. | ID | P87346 | |
| ID | Q03139 | AC | P87346 PRELIMINARY; PRT; 176 AA. | |
| DT | 01-NOV-1996 (TREMBLrel. 01, created) | | | |

AC P87346;
DT 01-MAY-1997 (TREMBLREL. 03, Created)
DT 01-MAY-1997 (TREMBLREL. 03, Last sequence update)
DT 01-NOV-1999 (TREMBLREL. 12, Last annotation update)
DE MYELIN BASIC PROTEIN.
OC Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;
Myelin.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN[J]; TISSUE[BRAIN];
RA NAGATA S.; OGINO K.;
RT "cDNA for Xenopus laevis myelin basic protein";
RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AB00736; BAA19174.1; -.
DR PRINTS: PRO0212; MYELINBMP.
KW Myelin.
SQ SEQUENCE 176 AA; 19720 MW; ABF3F06B CRC32;
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102 VARIANT A;
RA GOMPELS U.A., NICHOLAS J., LAWRENCE G., JONES M., THOMSON B.J.,
RT MARTIN M.E., ESTATHIOU S., CRAXTON M.A., GOMPELS U.A., HONESS R.W.,
RT "The DNA sequence of human herpesvirus-6: structure, coding content,
RT and genome evolution";
RL Virology 209:29-51(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102 VARIANT A;
RA MEDLINE: 90080132.
RL LAWRENCE G.L., CHEE M., CRAXTON M.A., GOMPELS U.A., HONESS R.W.,
RA BARRELL B.G.;
RT "Human herpesvirus 6 is closely related to human cytomegalovirus.>";
RL J. Virol. 64:287-299(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102 VARIANT A;
RA CHANG C.K., BALACHANDRAN N.;
RT "Identification, characterization, and sequence analysis of a cDNA
RT encoding a phosphoprotein of human herpesvirus 6.>";
RL J. Virol. 65:2884-2894(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE; 9133307.
RT TBO T.A., GRIFFIN B.E., JONES M.D.;
RL J. Virol. 65:4670-4680(1991).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE; 91226542.
RA THOMSON B.J., ESTATHIOU S., HONESS R.W.;
RT "Acquisition of the human adeno-associated virus type-2 rep gene by
RT human herpesvirus type-6.>";
RL Nature 351:78-80(1991).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE; 91374500.
RA MARTIN M.E.D., NICHOLAS J., THOMSON B.J., NEWMAN C., HONESS R.W.;
RT "Identification of a transactivating function mapping to the putative
RT immediate-early locus of human herpesvirus 6.>";
RL J. Virol. 65:5381-5390(1991).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE; 92333349.
RA ESTATHIOU S., LAWRENCE G.L., BROWN C.M., BARRELL B.G.;
RT "Identification of homologues to the human cytomegalovirus US22 gene
RT family in human herpesvirus 6.>";
RL J. Gen. Virol. 73:1661-1671(1992).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE; 92148942.
RA GENG Y., CHANDRAN B., JOSEPHS S.F., WOOD C.;
RT "Identification and characterization of a human herpesvirus 6 gene
RT segment that trans activates the human immunodeficiency virus type 1
RT promoter.>";
RL J. Virol. 66:1504-1510(1992).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE; 93091286.
RA GOMPELS U.A., CARSS A.L., SUN N., ARRAND J.R.;
RT "Infectivity determinants encoded in a conserved gene block of human
OS herpesvirus-6.>";
RT herpesvirus-6.);

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DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLREL. 08, Last annotation update)
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 RC STRAIN=U1102; VARIANT A;
 RX MEDLINE; 92260671.
 RA NEIPEL F., ELLINGER K., FLECKENSTEIN B.;
 RT "Gene for the major antigenic structural protein (p100) of human
 herpesvirus 6.;"
 RT J. Virol. 65:3918-3924(1992).
 RN [11] The right end of the unique region of the genome of human herpesvirus
 6 U1102 contains a candidate immediate early gene enhancer and a
 homologue of the human cytomegalovirus US22 gene family.;"
 RT J. Gen. Virol. 73:1649-1660(1992).
 RN [12] SEQUENCE FROM N.A.
 RP STRAIN=U1102; VARIANT A;
 RX MEDLINE; 93187613.
 RA ELLINGER K., NEIPEL F., FOA-TOMASI L., CAMPAGELLI-FIUME G.,
 RT "The glycoprotein B homologue of human herpesvirus 6.;"
 RA FLECKENSTEIN B.;
 RT [13] SEQUENCE FROM N.A.
 RC STRAIN=U1102; VARIANT A;
 RX MEDLINE; 93224882.
 RA GOMPELS U.A., CAFFIGAN D.R., CARSS A.L., ARNO J.,
 RT Two groups of human herpesvirus 6 identified by sequence analyses of
 RT laboratory strains and variants from Hodgkin's lymphoma and bone
 marrow transplant patients;"
 RT J. Gen. Virol. 74:613-622(1993).
 RN SEQUENCE FROM N.A.
 RP STRAIN=U1102; VARIANT A;
 RX MEDLINE; 93389439.
 RA LIU D.X., GOMPELS U.A., NICHOLAS J., LELLIOTT C.,
 RT "Identification and expression of the human herpesvirus 6 glycoprotein
 H and interaction with an accessory 40K glycoprotein.;"
 RT J. Gen. Virol. 74:1847-1857(1993).
 RN [14] SEQUENCE FROM N.A.
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 RC STRAIN=U1102; VARIANT A;
 RX MEDLINE; 94025558.
 RA LIU D.X., GOMPELS U.A., FOA-TOMASI L., CAMPAGELLI-FIUME G.,
 RT Human herpesvirus 6 glycoprotein H and L homologs are components of
 RT the gp100 complex and the gH external domain is the target for
 RT neutralizing monoclonal antibodies.;"
 RT Virology 197:112-22(1993).
 RN [15] SEQUENCE FROM N.A.
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 RX MEDLINE; 94025558.
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 RT Human herpesvirus 6 glycoprotein H and L homologs are components of
 RT the gp100 complex and the gH external domain is the target for
 RT neutralizing monoclonal antibodies.;"
 RT Virology 197:112-22(1993).
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 RA PELLET P.E., SANCHEZ-MARTINEZ D., DOMINGUEZ G., BLACK J.B., ANTON E.,
 RA GREENAMAYER C., DAMBANG T.R.;
 RT "A strongly immunoreactive virion protein of human herpesvirus 6
 RT variant B strain 229; identification and characterization of the gene
 RT and mapping of a variant-specific monoclonal antibody reactive
 RT epitope.;"
 RT Virology 195:521-531(1993).
 RN [17] SEQUENCE FROM N.A.
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 RC STRAIN=U1102; VARIANT A;
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 RA PFEIFFER B., BERNEMAN Z.N., NEIPEL F., CHANG C.K., TIRAWATNAPONG S.,
 RT CHANDRAN B.;
 RT "Identification and mapping of the gene encoding the glycoprotein
 complex gp85-gp100 of human herpesvirus 6 and mapping of the
 neutralizing epitope recognized by monoclonal antibodies.;"
 RT J. Virol. 67:4611-4620(1993).
 RN [18] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC STRAIN=U1102; VARIANT A;
 RX MEDLINE; 93146989.
 RA GOMPELS U.A., MACUTAY H.A.;
 RT "Characterization of human telomeric repeat sequences from human
 herpesvirus 6 and relationship to replication.;"
 RT J. Gen. Virol. 76:451-458(1995).
 RN [19] SEQUENCE FROM N.A.
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 RC STRAIN=U1102; VARIANT A;
 RX MEDLINE; 94047392.
 RA DEMURST S., DOLLARD S.C., PELETT P.E., DAMBAUGH T.R.;
 RT "Identification of a lytic-phase origin of DNA replication in human
 herpesvirus 6B strain 229.;"
 RT J. Virol. 67:6680-6683(1993).
 RN [20] SEQUENCE FROM N.A.
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 RA NICHOLAS J.;
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 RA NICHOLAS J., MARTIN M.;
 RT "Nucleotide sequence analysis of a 38.5-kilobase-pair region of the
 genome of human herpesvirus 6 encoding human cytomegalovirus
 immediate-early gene homologs and transactivating functions.;"
 RT J. Virol. 68:597-610(1994).
 RN [22] SEQUENCE FROM N.A.
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 RC STRAIN=U1102; VARIANT A;
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 RA SCHWEU U., NEIPEL F., SCHREINER D., FLECKENSTEIN B.;
 RT "Structure and transcription of an immediate-early region in the human
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 RT J. Virol. 68:2978-2985(1994).
 RN [23] SEQUENCE FROM N.A.
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 RX MEDLINE; 94181269.
 RA THOMPSON J., CHOUDHURY S., KASHANCHI F., DONIGER J., BERNEMAN Z.,
 RA FRENKEL N., ROSENTHAL I.J.;
 RT "A transforming fragment within the direct repeat region of human
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 GN U24
 OS Human herpesvirus 6.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Roscovirivirus.
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 RC STRAIN=IST;
 RA ISOGAWA Y., MUKAI T., NAKANO K., KAGAWA M., CHEN J., MORI Y.,
 RA SUNAGAWA T., SASHIKURA J., ZOU P., KOSUGI H., YAMANISHI K.,
 RA "A comparison of the complete DNA sequences between human herpesvirus-
 J. Virol. 67:4611-4620(1993)."

RT 6 variant A and B.;"
 RL J. Virol. 0-0-0-1999)
 DR EMBL; AB021506; BAA78245.1; -.
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 DT 01-NOV-1998 (TREMBLREL. 08, Last annotation update)
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 GN BOLF1.
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 OC Betaherpesvirinae; Roseolovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=01102;
 RC MEDLINE; 94118404.
 RA NICHOLAS J., MARTIN M.;
 RT "Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of human herpesvirus 6 encoding human cytomegalovirus immediate-early gene homologs and transactivating functions.";
 RT J. Virol. 68:597-610(1994).
 RL EMBL; L25528; AAH16738.1; -.
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 GN YMAG.
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 OC Bacillus/staphylococcus group; Bacillus.
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 RC STRAIN=168;
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 RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G., AZEVEDO V., BERTERO M.G., BESSIRE S.P., BOLOTIN A., BORGHERT S., BORRISSE R., BOURRIER L., BRANS A., BRAUN M., BRIGNTILL S.C., BRON S., BROUILLET S., BRUSCHI C.V., CALDWELL B., CAUANO V., CARTER N.M., CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A., DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T., ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D., FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,

RA GHIM S.Y., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G., GUISEPI G., GUY B.J., HAIECH J., HARWOOD C.R., HENAUT A., HILBERT H., HOISAPPAL S., HOSONO S., HULLIO M.F., ITAYA M., JONES L., JORIS B., KARAMATA D., KASAHARA Y., KLAIR-BLANCHARD M., KLEIN C., KOBAVASHI Y., KOETTER P., KONGNINGSTIN G., KROGH S., KUNANO M., KURITA K., LAPIDUS A., LARDINOLIS S., LAUBER J., LAZAREVIC V., LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C., MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M., NOONE D., O'REILLY M., OGAWA K., OGAWA A., OUDIGA B., PARK S.H., PARRO V., POHL T.M., POROTELLE D., PORMOLLIK S., PRESCOTT A.M., PRESCOTT E., PUJIC P., PURNELLE B., RAPORT G., REI M., REYNOLDS S., RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIKE Y., SATO T., SCANTLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F., RA SEKIGUCHI J., SEKOWSKA A., SEROR S.J., SEROR P., SHIN B.S., SOLDO B., SOKIN A., TACCONI E., TAGGI T., TAKAHASHI H., TAKEMARU K., TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTA P., TOGNONI A., TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A., VIARI A., WAMBUTT R., WEDLER E., WEDLER H., WEITZENEGGER T., WINTERS P., WIRTS A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A., "The complete genome sequence of the gram-positive bacterium Bacillus subtilis"; Nature 390:249-256(1997).
 RL Nature 390:249-256(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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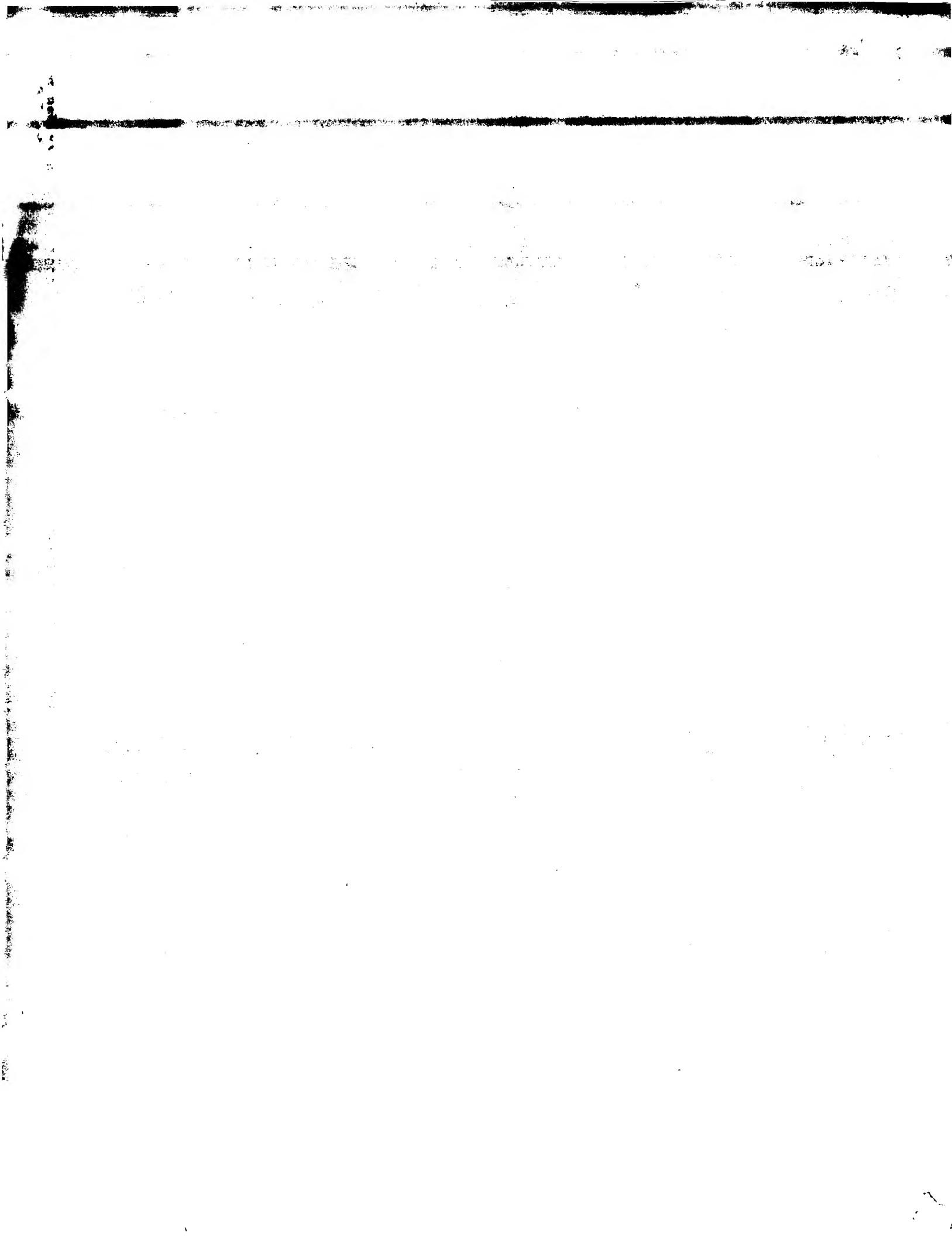
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us-09-218-277-12.rspt

Page 7



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About: Results were produced by the Gencore software, version 4.5,

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COMMENT        Email: smith@email.marc.usda.gov
JOURNAL        USDA, ARS, US Meat Animal Research Center, PO Box 156, Clay Center, NE 68933-0156, USA
COMMENT        Tel: 402 762 4366
COMMENT        Fax: 402 762 4390
COMMENT        Contact: Smith TPL
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AUTHORS        Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and Keele,J.W.
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 JOURNAL Unpublished (1999)
 COMMENT On May 18, 1998 this sequence version replaced gi:3137154.
 Contact: Katsuyuki Hashimoto
 Division of Genetic Resources
 National Institute of Infectious Diseases
 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 Email: khashi@nih.go.jp
 URL: <http://www.nih.go.jp/yoken/genbank/>

FEATURES Location/Qualifiers

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 /lab_host="TOP10"
 /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dt) primer [ATGGGCGCTTCTTTTCTTCTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTCGCCATCTG], digested and cloned into distinct DraIII sites of the pME18S-FL3. XbaI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTCTGCCTAAAGCGCG]"

BASE COUNT 165 YSerProMetAlaArgArg 171
 ORIGIN 537 ATCTCCCATGGCGAGACG 555

alignment_scores:

| Quality: | Length: | Ratio: | Gaps: | Percent Identity: |
|----------|---------|--------|-------|---------------------------------|
| 829.00 | 173 | 4.964 | 4 | 96.532 Percent Identity: 93.642 |

alignment_block:
 US-09-218-277-12 x AU079802 ..

Align seg 1/1 to: AU079802 from: 1 to: 808

1. MetAlaSerGlnLysArgProSerGinArgHisGlySerLysTyruEuaI 17
 ||||| ||||||| ||||||| ||||||| ||||| ||||| ||||| ||||| 17
 49 ATGGCACTCACAGAAGAAGACCTCAAGCGA.....TCCAGTACTGGC 92
 17 aThrAlaSerThrMetAspPhiSalArgHgIsglyPhiLeuProAqGHIsA 34
 ||||| ||||||| ||||||| ||||||| ||||| ||||| ||||| ||||| 34
 93 CACACAAAGTACATGGACCATGGCAGGCAAGCCTCCAAAGCACA 142
 34 RGAStPheGlyIleAspSerIleGlySerGlyPhiPhiHeGlyGlyAspArg 50
 ||||| ||||||| ||||||| ||||||| ||||| ||||| ||||| ||||| 50
 143 GAGACAGGGCATCTTGACTCCARGGGGCTTCTTACGGGACAGG 192
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="MNCB-1114"
 /clone_id="Sugano mouse brain mncb"
 /sex="female"
 /dev_stage="adult"
 /lab_host="TOP10"
 /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dt) primer [ATGGGCGCTTCTTTTCTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTCGCCATCTG], digested and cloned into distinct DraIII sites of the pME18S-FL3. XbaI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTCTGCCTAAAGCGCG]"

BASE COUNT 116 RTRPGLYALAGLUGIYLgInArgProGlyPhiGlyTyrglyVargAlas 133
 ORIGIN 387 CTGGGGGGCGAGGGAGCAGGCCAGGATTGGCTACGGAGGCAGCT 436

COMMENT 133 ERASPTyLysSerLahLysLysGlyPhiLysGlyVal..AspAlaGln 148
 On Oct 30, 1998 this sequence version replaced gi:3816313.
 Contact: Katsuyuki Hashimoto
 Division of Genetic Resources
 National Institute of Infectious Diseases
 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 Email: khashi@nih.go.jp
 URL: <http://www.nih.go.jp/yoken/genbank/>

FEATURES Location/Qualifiers

source

1. .811 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="MNCB-1114"
 /clone_id="Sugano mouse brain mncb"
 /sex="female"
 /dev_stage="adult"
 /lab_host="TOP10"
 /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dt) primer [ATGGGCGCTTCTTTTCTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTCGCCATCTG], digested and cloned into distinct DraIII sites of the pME18S-FL3. XbaI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTCTGCCTAAAGCGCG]"

BASE COUNT 116 RTRPGLYALAGLUGIYLgInArgProGlyPhiGlyTyrglyVargAlas 133
 ORIGIN 387 CTGGGGGGCGAGGGAGCAGGCCAGGATTGGCTACGGAGGCAGCT 436

alignment_scores:

| Quality: | Length: | Ratio: | Gaps: | Percent Identity: |
|----------|---------|--------|-------|---------------------------------|
| 821.00 | 173 | 4.946 | 4 | 95.954 Percent Identity: 93.064 |

alignment_block:
 100 ProProProSerGlnLysLysGlyArgGlyIleSerLeuSerArgPhes 116
 ||||| ||||||| ||||||| ||||||| ||||| ||||| ||||| ||||| 116
 237 TACCCATTATGGCTCTGGCCAGAGTCGACGCCAGCAAGTTAG 286
 83 SPGLAlaSerValWtIlePhiLysAsnIleIleWtIlePhiLys 99
 ||||| ||||||| ||||||| ||||||| ||||| ||||| ||||| ||||| 99
 287 ATGAAACACCAGTAGTCATTCATCTCAAGACATGTGACACTGACA 336
 337 CCACCCATCCACAGGAGGGAGGGCAGTCGCCCCACAGAATAG 386

seq_name: gb_est29:AU067209

seq.documentation_block:

LOCUS AU067209 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-3084

DEFINITION 5' mRNA sequence.

ACCESSION AU067209

VERSION AU067209.1 GI:4967946

KEYWORDS house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 827)

AUTHORS Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, A., Hirata, M., Suzuki, Y., Sasaki, M. and Sugano, S.

TITLE Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method

JOURNAL Unpublished (1999)

COMMENT On Jul 9, 1999 this sequence version replaced gi:5434934.

Contact: Katsuyuki Hashimoto

Division of Genetic Resources

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23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

Email: khashi@nih.go.jp

URL: http://www.nih.go.jp/yoken/genbank/.

FEATURES source

1. 827

/organism="Mus musculus"

/strain="C57BL"

/db_xref="txon:10090"

/clone="MNCB-3084"

/sex="female"

/dev_stage="adult"

/lab_host="TOP10"

/note="Organ: brain; Vector: PME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer [ATGGGCCGTCCTTGTGTTT] double-stranded cDNA was ligated to a DRAII adaptor [TCTTGGCCATCGG], digested and cloned into distinct DRAII sites of the PME18S-FL3. XbaI sites just outside the DRAII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTCTCGCTCTAAAGCTGGC]"

BASE COUNT 196 a 241 c 217 g 163 t 10 others

ORIGIN

alignment_scores:

| | | | |
|---------------------|--------|-------------------|--------|
| Quality: | 810.00 | Length: | 169 |
| Ratio: | 4.969 | Gaps: | 4 |
| Percent Similarity: | 96.450 | Percent Identity: | 93.491 |

align seg 1/1 to: AU067209 from: 1 to: 827

1 MetalaserGlyLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17

45 ATGGCATCACAGAGAGACCCTCACAGGA.....TCCAAGTACGCC 88

seq_name: gb_est29:AU067431

seq.documentation_block:

LOCUS AU067431 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-3446

DEFINITION 5' mRNA sequence.

ACCESSION AU067431

VERSION AU067431.1 GI:4968168

KEYWORDS house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 720)

AUTHORS Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, A., Hirata, M., Suzuki, Y., Sasaki, M. and Sugano, S.

TITLE Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method

JOURNAL Unpublished (1999)

COMMENT On Oct 8, 1998 this sequence version replaced gi:3727975.

Contact: Katsuyuki Hashimoto

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National Institute of Infectious Diseases

23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

Email: khashi@nih.go.jp

URL: http://www.nih.go.jp/yoken/genbank/.

FEATURES source

1. 720

/organism="Mus musculus"

/strain="C57BL"

/db_xref="txon:10090"

/clone="MNCB-3446"

/sex="female"

/dev_stage="adult"

/lab_host="TOP10"

/note="Organ: brain; Vector: PME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer [ATGGGCCGTCCTTGTGTTT] double-stranded cDNA was ligated to a DRAII adaptor [TCTTGGCCATCGG], digested and cloned into distinct DRAII sites of the PME18S-FL3. XbaI sites just outside the DRAII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTCTCGCTCTAAAGCTGGC]"

BASE COUNT 196 a 241 c 217 g 163 t 10 others

ORIGIN

alignment_scores:

| | | | |
|---------------------|--------|-------------------|--------|
| Quality: | 810.00 | Length: | 169 |
| Ratio: | 4.969 | Gaps: | 4 |
| Percent Similarity: | 96.450 | Percent Identity: | 93.491 |

align seg 1/1 to: AU067209 from: 1 to: 827

1 MetalaserGlyLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17

45 ATGGCATCACAGAGAGACCCTCACAGGA.....TCCAAGTACGCC 88

/sex="female"
 /dev_stage="adult"
 /lab_host="TOP10"
 note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
 was primed with an oligo(dt) primer
 [ATGGCCGCTTGTGTTTGTGTT] double-stranded cDNA was
 ligated to a DRAII adaptor [TGTTGCCCTACCGG] , digested
 and cloned into distinct DRAII sites of the pME18S-FL3.
 XbaI sites just outside the DRAII sites can be used to
 isolate the cDNA insert. Size selection was performed to
 exclude fragments <1.5 kb. Library was constructed by
 Sugano et al. (University of Tokyo, Institute of Medical
 Science). Custom primer for sequencing: 5' end primer
 [CTCTGCCTCTAAAGCTGCG]"
 BASE COUNT 178 a 222 c 186 g 132 t 2 others
 ORIGIN

alignment_scores:
 Quality: 807.00 Length: 174
 Ratio: 4.861 Gaps: 5
 Percent Similarity: 95.402 Percent Identity: 92.529

alignment_block:
 US-09-218-277-12 x AU067431 ..

Align seg 1/1 to: AU067431 from: 1 to: 720

1 MetAlaserGlnLysArgProSerGlnArgHisGlySerIleTyrLeuAl 17
 |||||||.....|||||||.....|||||||.....|||||||.....|||||||
 55 ATGGCATACAGAGAGGCCCTACAGCGA.....TCCAGTACTGGC 98
 17 athralaserThrMetAspHisAlaGlyGlySerIleLeuProArgHisA 17
 |||||||.....|||||||.....|||||||.....|||||||.....|||||||
 99 CACAGCAAGTACCATGGACCATGGCTTCGCCAACGGCACA 148
 34 rAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
 |||||||.....|||||||.....|||||||.....|||||||.....|||||||
 149 GAGACACGGCAGCTCTGACTCCATGGGGCTCTTTCGGGACAGG 198
 51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgH 67
 |||||||.....|||||||.....|||||||.....|||||||.....|||||||
 199 GGTCGCCCAAGGGGCTCTGGCAAGGCTCACAC.....ACGAAAC 242
 67 RalaHistTygGlySerLeuProGlnLysSer..HisGlyArgThrGlnA 83
 |:::|||||.....|||||||.....|||||||.....|||||||.....|||||||
 243 TACCCATPATGGCCCGGCCAGAATGGCGCACGCCGGACCAAG 292
 83 spGluAsnProValValHisPhePheLysAsnIleLeuThrProArgThr 99
 |||||||.....|||||||.....|||||||.....|||||||.....|||||||
 293 ATGAAACCCAGTAGTCATTCTCAAGAACATGTGACACTCGACA 342
 100 ProProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSe 116
 343 CCACCTCCATCCAAAGGAGGGAGGGAGGAGCTGTCCTCAGCACATTAG 392
 BASE COUNT 193 a 232 c 198 g 158 t 19 others
 ORIGIN

alignment_scores:
 Quality: 807.00 Length: 174
 Ratio: 4.861 Gaps: 5
 Percent Similarity: 95.402 Percent Identity: 92.529

alignment_block:
 US-09-218-277-12 x AU051764 ..

Align seg 1/1 to: AU051764 from: 1 to: 800

1 MetAlaserGlnLysArgProSerGlnArgHisGlySerIleTyrLeuAl 17
 |||||||.....|||||||.....|||||||.....|||||||.....|||||||
 48 ATGGCTCACAGAGAGACCTCACAGCGA.....TCCAGTACTGGC 91
 17 athralaserThrMetAspHisAlaGlyGlySerIleLeuProArgHisA 34
 |||||||.....|||||||.....|||||||.....|||||||.....|||||||
 92 CACAGGAAGTACCATGGACCATGGCAGGGCCTCTTCAGGTCAGCAGG 141
 34 rAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
 |||||||.....|||||||.....|||||||.....|||||||.....|||||||
 142 GAGACACGGCAGCTCTGACTCCACGGGCGCTCTTASGGTGAAGCAGG 191

seq_documentation_block:
 LOCUS AU051764 mRNA EST 18-MAR-1999
 DEFINITION AU051764 Sugano mouse brain mncc Mus musculus cDNA clone MNCCb-2446
 5', mRNA sequence.

REFERENCE AU051764.1 GI:4434773

VERSION AU051764.1

KEYWORDS EST.

ORGANISM house mouse.

SOURCE Mus musculus

AUTHORS Eukarrota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Sakai,M., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K.,
 Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.

TITLE Construction of mouse full length-enriched cDNA libraries by
 oligo-capping

JOURNAL Unpublished (1999)

COMMENT On Feb 22, 1999 this sequence version replaced gi:4283685.
 Contact: Katsuyuki Hashimoto
 Division of Genetics
 National Institute of Infectious Diseases
 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 Email: khashi@nih.go.jp
 URL: http://www.nih.go.jp/yoken/genbank/

FEATURES Seq primer: 5' end primer: CTTCCTCTCTAAAGCTGCG.
 source Location/Qualifiers

1. . 800

/organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:1090"
 /clone="MNCCb-2446"
 /clone_1.lib="Sugano mouse brain mncc"
 /sex="female"
 /dev_stage="adult"
 /lab_host="TOP10"
 /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
 was primed with an oligo(dt) primer
 [ATGGCCGCTTGTGTTTGTGTT] double-stranded cDNA was
 ligated to a DRAII adaptor [TGTTGCCCTACCGG] , digested
 and cloned into distinct DRAII sites of the pME18S-FL3.
 XbaI sites just outside the DRAII sites can be used to
 isolate the cDNA insert. Size selection was performed to
 exclude fragments <1.5 kb. Library was constructed by
 Sugano et al. (University of Tokyo, Institute of Medical
 Science). Custom primer for sequencing: 5' end primer
 [CTCTGCCTCTAAAGCTGCG]"

| | | |
|--|--|---|
| | | Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTTCGCTCTAAAGCTGGC]". |
| BASE COUNT | 189 a | 223 c |
| ORIGIN | 203 g | 153 t |
| | 11 others | |
| alignment_scores: | Quality: 776.00 | Length: 169 |
| Percent Similarity: | 4.790 | Gaps: 4 |
| Percent Identity: | 95.858 | Percent Identity: 92.899 |
| alignment_block: | US-09-218-277-12 x AU035931 | .. |
| Align seg 1/1 to: AU035931 from: 1 to: 779 | | |
| 1 METALaserGlyIysAqPProSrglarnghslySerlystyLeual | : : : : : : : : : | 17 |
| 49 ATGCGATCATCACAGAGACCCCTACACCGGA.TCCAAGTACCTGC | : : : : : : : : : | 92 |
| 17 arthalaserthermMetaphisAlarHisGlyPheleuproArgHsA | : : : : : : : : : | 34 |
| 93 CACAGCAAGTACCATGGACCATGCCAGGATGCTTCCTCCANGACA | : : : : : : : : : | 142 |
| 34 rgsptgIyIileLeuspsellieglyArgphephglyIyAsparg | : : : : : : : : : | 50 |
| 143 GAGACACGGGCATCTGACTCTGACTCTCACGGCGCTTCTAGGGGACAG | : : : : : : : : : | 192 |
| 51 GlyAlaProllysArgIysGlyArglylysAspSerHishisProAlargin | : : : : : : : : : | 67 |
| 193 GRRGCGGCCAASCGGGSCTCTGGCAAGGACTCACAC.ACGAGAAC | : : : : : : : : : | 236 |
| 67 ralahlstyryGlySerLeuProGlnLsSer... HisGlyArgThrGlna | : : : : : : : : : | 83 |
| 237 TACCCATTATGGCTCCCTGCCAGAACCTGGCACACGGCCGACCG | : : : : : : : : : | 286 |
| 83 spgluAspProValValHisPhephlylysAsnilevalThrProArgThr | : : : : : : : : : | 99 |
| 287 ATGAAACCCAGTACGTCCATTCTCTCAAGAACATGTGACACCCTGAACA | : : : : : : : : : | 336 |
| 100 PROPROProSerGlyIlySerlyArglylysAspSerHishisProAlargin | : : : : : : : : : | 116 |
| 337 CCACCTCCATCCCAGGGAGGGAGAGGCCCTGCCCTCAGCAGATTG | : : : : : : : : : | 385 |
| 116 rtrpglyIalagluglyIyArgProGlyPhegyTyrglyIyArgAlas | : : : : : : : : : | 133 |
| 387 CTGGGGGGCGAGGGCAGAGCCAGGATTTGGCTACGGAGGAGAGCTT | : : : : : : : : : | 435 |
| 133 erasptylysserAlahislygIylyphephlyIyArglyIyArgAlas | : : : : : : : : : | 133 |
| 437 CGACTATATACTGGCTCACAGGATCAAGGGCCCTACGGGCCAG | : : : : : : : : : | 485 |
| 149 GlyThrLeuSerlyIlePhelysLeuglyIyArgAspSerArgSerI | : : : : : : : : : | 165 |
| 487 GGACAGCTTTC. AAACTCTTAAGCTGGGAGGAAGACAGCCCTCTGG | : : : : : : : : : | 535 |
| 165 Yser-Pro 167 | : | 536 ATCCTCA 542 |
| source | ORGANISM: Mus musculus | |
| RES | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; | |
| source | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | |
| INT | 1 (bases 1 to 779) | |
| ENCE | Sasaki.Z., Suzuki.Y., Watanabe.M., Imai.J., Shibusawa.K., Hatta.H., Yamagishi.S. and Sugano.S. | |
| HORS | Construction of mouse full length-enriched cDNA libraries | |
| LE | Unpublished (1998) | |
| RNAL | Contact: Katsuyuki Hashimoto | |
| INT | Division of Genetic Resources | |
| NT | National Institute of Infectious Diseases | |
| 231 - Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan | Email: khashi@nih.go.jp. | |
| Location/Qualifiers | /sex="female" | |
| 1. 779 | /organism="Mus musculus" | |
| /strain="C57BL" | /db_xref="taxon:10990" | |
| /clone="MNCB-1058" | /clone.lib="Sugano mouse brain mncb" | |
| /dev_stage "adult" | /dev_stage "adult" | |
| /lab_host="Tohoku" | /lab_host="Tohoku" | |
| /note="Organism: brain; Vector: PME18S-FL3; 1st strand cDNA was primed with an Oligo(dT) primer [ATGGCCGTTTTTTTTTTTT] double-stranded cDNA was ligated to a BRL11 adaptor [TGTTGCCCTACTGG], digested and cloned into distinct BRL11 sites of the PME18S-FL3. XbaI sites just outside the BRL11 sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 Kb. Library was constructed by | seq_documentation_block: | |
| | LOCUS AU051348 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-1908 | |
| DEFINITION | 5', mRNA sequence. | |
| VERSION | AU051348.1 GI:4434357 | |
| KEYWORDS | EST. | |
| SOURCE | house mouse. | |
| ORGANISM | Mus musculus | |

REFERENCE
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
(bases 1 to 804)
Sasaki,M., Suzuki,Y., Watanabe,M., Imai,J., Shibusawa,A., Yoshioka,K.,
Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S. libraries by
construction of mouse full length-enriched cDNA libraries by
oligo-capping.
Unpublished (1999)

COMMENT
On Jun 5, 1998 this sequence version replaced 91:3187684.
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
URL: <http://www.nih.go.jp/yoken/genbank/>

FEATURES
source
I. . 804
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="MNcb-1908"
/clone_libr="Sugano mouse brain mncb"
/sex="Female"
/dev_stage="adult"
/lab_host="TOP10"
/note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
was primed with an oligo(dT) primer
[ATGGCCCTTTTTTTTTTT] double stranded cDNA was
ligated to a DRAII adaptor [TGTTGCCCTACGGGCTACGAGCCAG 484
and cloned into distinct DRAII sites of the pME18S-FL3.
XbaI sites just outside the DRAII sites can be used to
isolate the cDNA insert. Size selection was performed to
exclude fragments <1.5 kb. Library was constructed by
Sugano et al. (University of Tokyo, Institute of Medical
Science). Custom primer for sequencing: 5' end primer
[CTCTGCCTAAAGCTCGG]" 165
a 204 c 176 g 176 t 58 others
alignment_scores:
Quality: 775.00 Length: 174
Ratio: 4.784 Gaps: 15
Percent Similarity: 93.103 Percent Identity: 89.080
alignment_block:
BASE COUNT ORIGIN
190 a 204 c 176 g 176 t 58 others
a1gn seg 1/1 to: AU051348 from: 1 to: 804
1 NetAlaSerGlnLysArgProSerGlnArgHisGlySerLysNleAla 17
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 1
47 ATGGCATCACAGAAGAGACCCACAGCGA....TCCAAGTACCTGGC 90
17 sThrAlaSerThrMetAspPheAlaAlaGlyGlyPheLeuProArgHisA 34
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 1
91 CACACGAACTTACCATGGACCATGCCAGGCAAGCTCTCCCAAGGACA 140
34 RgAspPheGlyTleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
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141 GAGACACGGGAACCTGTACCTACCGGGCTCTTAGGGTGAAGG 190
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 1
51 GlyAlaProLysArgSerGlySerLysAspSerPheHisPheAlaArgTh 67
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191 GGTGCGCCAACGGGGCTCTGGCAAGACTACAC....ACGAGAC 234
67 RalaHisTyrglySerIleProGlnLysSer..HisGlyArgThrGlnA 83
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 1
235 TACCCATTATGCTCCGCCCCAGAAGTCGCCAGACGCCGACCCAG 284
83 SPGLuSNPrOValValHisPhePhelysAspIleValThrProArgThr 99
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 1
285 ATGAAACCCACTAGTCATCTTCAGACATTTGACACCTCGCAAC 334

FEATURES
source
I. . 771
seq_documentation_block:
LOCUS AU066115 mRNA EST 02-JUN-1999
DEFINITION AU066115 Sugano mouse brain mncb Mus musculus cDNA clone MNcb-2602
ACCESSION AU066115
VERSION AU06615.1 GI:4967552
KEYWORDS EST
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Hashimoto,K., Kisuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M.,
Suzuki,I., Sasaki,M. and Sugano,S.
TITLE Isolation of full-length cDNA clones from a mouse brain cDNA
library made by Oligo-capping method
COMMENT Unpublished (1999)
On Apr 7, 1998 this sequence version replaced 91:3036368.
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
URL: <http://www.nih.go.jp/yoken/genbank/>.

FEATURES
source
I. . 771
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="MNcb-2602"
/clone_libr="Sugano mouse brain mncb"
/sex="Female"
/dev_stage="adult"
/lab_host="TOP10"
/note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
was primed with an oligo(dT) primer
[ATGGCCCTTTTTTTTT] double stranded cDNA was
ligated to a DRAII adaptor [TGTTGCCCTACGGGCTACGG 484
and cloned into distinct DRAII sites of the pME18S-FL3.
XbaI sites just outside the DRAII sites can be used to
isolate the cDNA insert. Size selection was performed to
exclude fragments <1.5 kb. Library was constructed by
Sugano et al. (University of Tokyo, Institute of Medical
Science). Custom primer for sequencing: 5' end primer
[CTCTGCCTAAAGCTCGG]" 165
a 187 c 219 g 199 t 14 others
alignment_scores:

425 CTGACTACAAACCGCTCACAGGACTCAAGGGGCCAGGACGCCAG 474
 149 GlyThrLeuSerLysIlePhenLeuIle 157
 475 GGCACACTTCCAAATCTCAAGCTG 501

seq_name: gb_est29:AU080522

seq_documentation_block:

LOCUS AU080522 Sugano mouse brain mncb Mus musculus EST 20-OCT-1999
 DEFINITION AU080522 Sugano mouse brain mncb Mus musculus cDNA clone MNcb-5756
 VERSION AU080522
 KEYWORDS EST

JOURNAL house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (bases 1 to 782)

AUTHORS Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, A., Hirata, M.,
 Suzuki, Y., Sasaki, M. and Sugano, S.

TITLE Isolation of full-length cDNA clones from a mouse brain cDNA
 library made by oligo-capping method
 Unpublished (1999)
 On Jul 7, 1999 this sequence version replaced gi:5408331.

COMMENT Contact: Katsuyuki Hashimoto
 Division of Genetic Resources
 National Institute of Infectious Diseases
 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 Email: khashi@nih.go.jp
 URL: <http://www.nih.go.jp/yoken/genbank/>.

FEATURES source

1. .782

/organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone_id="MNcb-5756"
 /sex="female"
 /dev_stage="adult"
 /lab_host="TOPIO"
 /note="Organ: brain; Vector: PME18S-FL3; 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGGGCCCTTTTCTTCTTCTT] double-stranded cDNA was
 ligated to a BTAII adaptor [TGTTGCCCTAATGG], digested
 and cloned into distinct BTAII sites of the PME18S-FL3.
 XbaI sites just outside the BTAII sites can be used to
 isolate the cDNA insert. Size selection was performed to
 exclude fragments <1.5 kb. Library was constructed by
 Sugano et al. (University of Tokyo, Institute of Medical
 Science). Custom primer for sequencing: 5' end primer
 [CTTCGCTCTAAACCTGGC]"

BASE COUNT 205 a 213 c 205 g 154 t 5 others

ORIGIN

alignment_scores:

| | | | |
|----------|--------|---------|-----|
| Quality: | 753.00 | Length: | 166 |
| Ratio: | 4.827 | Gaps: | 164 |

Percent Similarity: 93.976 Percent Identity: 89.157

alignment_block: US-09-218-277-12 x AU080522 ..

Align seq 1/1 to: AU080522 from: 1 to: 782

FEATURES source

1. .770

/organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone_id="MNcb-2726"
 /sex="female"
 /dev_stage="adult"
 /lab_host="TOPIO"
 /note="Organ: brain; Vector: PME18S-FL3; 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGGGCCCTTTTCTT] double-stranded cDNA was

339 CACAGCAAGTACCATGGACCAGATGCCAGCATGCTTCTCCAAAGCACA 388
 34 RASPTHGLYIleLeuAspSerIleGlyArgPheGlyAspArg 50
 389 GAGACAGGGCATCTGTACTCATGGGCCCTCTTAGGGTGCAGG 438
 51 GlyAlaProLysArgGlySerGlySerGlyAspSerHisProAlaRGTh 67
 439 GGTGCGCCAAAGGGCTCTGCAAGGACTCACAC.....ACGAGAAC 482
 67 RIAAHISItyrglyserieuPrGlnysser...HisGlyArgTglna 83
 483 TACCCATTATGCTCCCTGCCAGAACGAGTCCGACAGCAGGCCAG 532
 83 SPGLuLAsPVALVAlValHispPhelysAsnLysValThrProArgThr 99
 533 RTGAAACCCAGTAGTCATTCCTCAAGAACATGtgACACTGGAACA 582
 100 ProProProSerGlnGlyLsGlyArgGlyLeuSerLeuSerArgPheSe 116
 583 CCACTTCATCCAGGAAGGGAGAGGCCGTCGTCCTCAGGATTAG 632
 116 RTGPGlyAlaGlyGlyGlyGlnArgProDlyPheGlyTgryGlyArgAla 133
 633 CTTGGGGGCCGAGGGCANAAAGCCAGGATGCTACNGAGGAGCTT 682
 133 EAStPThIySSerAlaHispGlyPhelysGlyVal..AspAlaGln 148
 683 NGAGACTATAATGGNtCACAGGGATCAAGGGGCTACAGGCCAG 732
 149 GlyThrLeuSerLysIlePhelysLsGlyArgGlyLeuSerLeuSerArgPheSe 164
 733 GCACGCTTTCAAACTCTTAACTGGGANGAAGAACAGCCGNCT 780

seq_name: gb_est29:AU066924

seq_documentation_block:

LOCUS AU066924 Sugano mouse brain mncb Mus musculus EST 02-JUN-1999
 DEFINITION AU066924 Sugano mouse brain mncb Mus musculus cDNA clone MNcb-2726
 VERSION AU066924
 KEYWORDS EST

JOURNAL house mouse.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (bases 1 to 770)

AUTHORS Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, A., Hirata, M.,
 Suzuki, Y., Sasaki, M. and Sugano, S.

TITLE Isolation of full-length cDNA clones from a mouse brain cDNA
 library made by oligo-capping method
 Unpublished (1999)
 On Apr 7, 1998 this sequence version replaced gi:3036477.

COMMENT Contact: Katsuyuki Hashimoto
 Division of Genetic Resources
 National Institute of Infectious Diseases
 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 Email: khashi@nih.go.jp
 URL: <http://www.nih.go.jp/yoken/genbank/>.

1 MetAlaSerGlnIysArgProSerGlnArgHisGlySerLysTyrLeuAla 17
 295 ATGGCACTTCCAAATCTCAAGCTG.....TCCAAGTACCTGGC 338
 17 atraAlaSerIleMetAspHisLysGlyIleLeuProArgHsA 34

| VERSION | AA352612.1 | EST | G1:2004932 |
|---|---|--------------------------|------------|
| KEYWORDS | EST- human. | SOURCE | |
| ORGANISM | Homo sapiens | AUTHORS | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo. | FEATURES | |
| 1 (bases 1 to 511) | | Source | |
| Align seg 1/1 to: AA066924 from: 1 to: 770 | | BASE COUNT | 184 |
| 1 MetalaesarginylsArgProserglnArgHisGlySerlysTyrLeuAl 17 | | ORIGIN | a 225 |
| 48 ATGCATCAGCAGAGACCCCTCACAGCA.....TCCAGTACTGGC 91 | | alignment_block: | c 201 |
| 17 athrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34 | | Quality: 750.50 | g 151 |
| 92 CAAGCAGCAGTACCATGGACATGCCAGGATGGCTCCCTCCAAGCACA 141 | | Length: 173 | t 9 others |
| 34 rgasprhrglyIleIeuAspSerIleGlyIgrygPhephegyIgylasparg 50 | | Gaps: 5 | |
| 142 GAGACACGGGCATCCATGGGGCTCTTTAGGGTGACAG 191 | | Percent Identity: 86.705 | |
| 51 GlyIlaProIysArgGlySerGlyIysAspSerHishisProIaArgth 67 | | alignmentscores: | |
| 192 GTGTCGCCCAAGCGGGCTCTGGCAGGACTCACAC.....ACCGAAC 235 | | Quality: 750.50 | |
| 83 SPGLIaasnrovAlaValIhsPhepheIyLysAsnIleValIhrProArgThr 99 | | Length: 173 | |
| 286 ATGAArACCAGTAGTCATTCTCAAGACATGTGACACTCGACA 335 | | Gaps: 5 | |
| 100 ProProProserGlyIgrygIgylIleuSerLeuSerArgPhese 116 | | Percent Identity: 90.173 | |
| 336 CCACTCCATCCCAAGGGAAG..... 356 | | alignmentscores: | |
| 116 RTRPGlyIaIgIgLyIgIaIgIgProGlyPheglyTyrglyIgIyArgAlas 133 | | Quality: 749.00 | |
| 357 ...GGGGCGCAGGGCAGAGCCAGGATTTGGCTACGGAGGCCAG 402 | | Length: 160 | |
| 133 ERASPTYRLySSerIaLahIlySlyPhelysGlyIval..AspAlaGln 148 | | Gaps: 2 | |
| 403 CGCACTATAAAKICGGCTCACAGGGATTCAAGGGGCTACAGCGCCAG 452 | | Percent Identity: 93.750 | |
| 149 GlyTyrIleSerLysIlePhelLysIeGlyIaIgAspSerArgSerG1 165 | | alignmentscores: | |
| 453 GGCAAGCTTTCACAAATCTTTAAGCTGGGAGGAGACACCGCCTGG 502 | | Quality: 749.00 | |
| seq_documentation_block: | | Length: 160 | |
| LOCUS AA352612 511 bp mRNA EST 21-APR-1997 | | Gaps: 2 | |
| DEFINITION ESTm6032 Activated T-cells XX Homo sapiens cDNA 5' end similar to myelin basic protein, mRNA sequence. | | Percent Identity: 89.375 | |
| ACCESSION AA352612 | | alignmentscores: | |
| seq_name: gb.est6.AA352612 | | Quality: 749.00 | |
| 165 YSerProMetAlaIgarg 171 | | Length: 160 | |
| 503 ATCTTCCATGGGAGACGC 521 | | Gaps: 2 | |
| Align seg 1/1 to: AA352612 from: 1 to: 511 | | Percent Identity: 89.375 | |
| 1 MetalaesarginylsArgProserglnArgHisGlySerlysTyrLeuAl 17 | | alignmentscores: | |
| 35 AGGGCGCACAGAGAACCTCCCAAGGACAGGNTCCAAGTACCTGGC 85 | | Quality: 749.00 | |
| 17 athrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34 | | Length: 160 | |
| 86 CAGCAAGTACCATGGACCATGCCAGGCATGGCTCTCCCRAGGACCA 135 | | Gaps: 2 | |
| 34 rasprhrglyIleIeuAspSerIleGlyIgrygPhephegyIgylasparg 50 | | Percent Identity: 89.375 | |

||||||||||| |||||||||||||||||||||||
136 GAGACACGGGCATCNTTGACTCCATCGGGCTTCTTGGCGGTGACAGG 185
51 GLYALAPROLYSARGLYSERGLYLYSASPHERHISPROALAARGH 67
|||||||||:::|||||||||||||||||||||:
185 GGTGCCCTATCGGCGTCGGCAGGACNACACCCGGCAAGAAC 235
67 RLAHISTYRGYLSERIEUPROGLYLYSSERHISGYARGTHRGINASPG 84
|||||||||:
236 TGCTCACTATGCTCCCTGCCCAAGAGTACACGCCGACCCAGATG 285
84 IuAsnProValValHisPheHeLeuAsnIleValThrProAlaGlyPro 100
|||||||||:
286 AAAACCCCGTAGTCCACTCTTCAGACATNTGAGCCCTNGCACACCA 335
101 PROProSerGlyLysGlyArgGlyLeuSerLeuSerArgPhsSerR 117
|||||:
336 CCCCCCTNGCAGGAAAGGGAGGAGACTGCCCCTGAGCAGATTAGCTG 385
117 PGlyAlaGluGlyGlyGlyArgProGlyPheGlyArgGlyArgAlaSerA 134
|||||:
436 GGGGCCGAANAGTAGSNACCAGGATTITGGCTACGGAGGCGAGGTCCG 435
134 SPTYRLysSerAlaHsLysGlyPhesGlyVal AspAlaGlyLysTh 150
|||||:
436 ACTATAATCGGNTCAAAAGGGTCAAGGGAGTTCGATGNCAGGGNAC 485
150 r.LeuSerLsIlePhePheLysLeuGly 158
| :|||:
486 GTTTCAAAATTTTAAGCTGG 511

| OM protein - protein search, using sw model | | | | | | |
|--|-------|-------------|--------|----------|--|--|
| Run on: September 26, 2000, 17:47:28 ; Search time 40.8 Seconds | | | | | | |
| Title: US-09-218-277-12 | | | | | | |
| Perfect score: 922 | | | | | | |
| Sequence: 1 MASQKRPSSORGSKYLATAS.....SKIFKLGGRDSDRSQSGMARR | | | | | | |
| scoring table: BioSUM62 | | | | | | |
| Gapext 10.0 , Gapext 0.5 | | | | | | |
| Searched: 188963 seqs, 23686106 residues | | | | | | |
| total number of hits satisfying chosen parameters: 188963 | | | | | | |
| Minimum DB seq length: 0 | | | | | | |
| Maximum DB seq length: 200000000 | | | | | | |
| Post-processing: Minimum Match 0% | | | | | | |
| Maximum Match 100% | | | | | | |
| Listing first 45 summaries | | | | | | |
| Database : A_Genesedq_36:* | | | | | | |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | | |
| SUMMARIES | | | | | | |
| Result No. | Score | Query Match | Length | DB ID | Description | |
| 1 | 922 | 100.0 | 171 | 1 R97627 | Human myelin basic | |
| 2 | 922 | 100.0 | 171 | 1 R95580 | Human myelin basic | |
| 3 | 917 | 99.5 | 170 | 1 R48592 | Human myelin basic | |
| 4 | 917 | 99.5 | 170 | 1 R95406 | Myelin oligodendrocyte basic protein | |
| 5 | 909 | 98.6 | 170 | 1 R95440 | Human basic myelin | |
| 6 | 899 | 97.5 | 197 | 1 W00399 | Human myelin basic protein | |
| 7 | 899 | 97.5 | 203 | 1 W06107 | Poletal myelin basic protein | |
| 8 | 899 | 97.5 | 203 | 1 W06108 | Poletal myelin basic protein | |
| 9 | 899 | 97.5 | 373 | 1 W06103 | MP2 chimaera (MBP211) | |
| 10 | 899 | 97.5 | 385 | 1 W06102 | MP3 chimaera (MBP211) | |
| 11 | 899 | 97.5 | 492 | 1 W06105 | MPQGP4 chimaera (MBP211) | |
| 12 | 894 | 97.0 | 375 | 1 W06104 | MP4 chimaera (delta) | |
| 13 | 891 | 96.6 | 170 | 1 R0736 | Human MBP. Pure man | |
| 14 | 855 | 92.7 | 168 | 1 R04717 | Empirically determined rabbit myelin basic protein | |
| 15 | 832 | 90.2 | 168 | 1 R8594 | Rabbit myelin basic protein | |
| 16 | 822 | 89.2 | 169 | 1 R48593 | Cattle myelin basic protein | |
| 17 | 814.5 | 88.3 | 226 | 1 R8595 | Myelin basic protein | |
| 18 | 814.5 | 88.3 | 170 | 1 R30735 | Bovine MBP. Pure m | |
| 19 | 814.5 | 88.3 | 170 | 1 W07236 | Myelin basic protein | |
| 20 | 798.5 | 86.5 | 170 | 1 R86422 | Myelin basic protein | |
| 21 | 797.5 | 86.5 | 170 | 1 R45947 | Myelin basic protein | |
| 22 | 779.5 | 84.5 | 167 | 1 R48595 | Myelin basic protein | |
| 23 | 655 | 65.5 | 127 | 1 R48596 | Rat myelin basic protein | |
| 24 | 534 | 57.9 | 170 | 1 R48597 | Chicken myelin basic protein | |
| 25 | 260 | 28.2 | 46 | 1 W02360 | Human myelin basic protein | |
| 26 | 162 | 17.6 | 32 | 1 R85138 | Human MBP residues 133-170 | |
| 27 | 162 | 17.6 | 32 | 1 R95369 | Residues 111-135 of bovine MBP-2.5 (80-100). | |
| 28 | 140 | 15.2 | 25 | 1 R95367 | Human myelin basic protein | |
| 29 | 139 | 15.1 | 25 | 1 W03948 | MBP-5 (101-125). Myelin basic protein | |
| 30 | 139 | 15.1 | 25 | 1 R85347 | Human myelin basic protein | |
| 31 | 136 | 14.8 | 25 | 1 W03953 | Myelin basic protein | |
| 32 | 136 | 14.8 | 25 | 1 R9336 | Myelin basic protein | |
| 33 | 14.6 | 24 | 1 | | | |

| | |
|-------------|--|
| KW | experimental allergic encephalomyelitis; EAE; analogue. |
| OS | Homo sapiens. |
| PN | W0961086-A1. |
| PD | |
| PP | 16-NOV-1995; U14403; |
| PR | 18-NOV-1994; US-342408. |
| PA | (NEUR-) NEUROCRINE BIOSCIENCES INC. |
| PI | Conlon P, Gaur A, Ling N, Steinman L; |
| DR | WPI; 96-26835/27. |
| DR | DR-PSDB; T3561. |
| PT | Peptide analogues of human myelin basic protein - useful for treatment of multiple sclerosis disclosure; Figure 1; 61pp; English. |
| PS | Peptide analogues comprising at least seven amino acids from residues 86-99 of human myelin basic protein (MBP), can be used to treat multiple sclerosis by competing for the binding of native MBP peptide to MHC and by not causing proliferation of an MBP reactive T-cell line. The peptide analogues also inhibit the induction of experimental allergic encephalomyelitis (EAE) by MBP in rodents. |
| CC | The peptide analogues have a reduced susceptibility to proteolysis in vivo. |
| CC | Sequence 171 AA: |
| Query Match | 99.5%; Score 917; DB 1; Length 170; |

QY 62 HRPARTAHYGSLLPKSHGRTODENPVHFFRNIVPRTPPPSQGKGRLSLSRFSGAEG 121
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 ID W00399 standard; Protein: 197 AA.
 Db HHPARTAHYGSLLPKSHGRTODENPVHFFRNIVPRTPPPSQGKGRLSLSRFSGAEG 120
 AC W00399;
 DE 01-FEB-1997 (first entry)
 KW Human myelin basic protein (foetal isoform).
 OS Myelin basic protein; MBP; MBP+X2cys81; proteolipid protein; PLP;
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;
 T-lymphocyte; T-cell; anergy; apoptosis.
 OS Homo sapiens.

RESULT 5 R35440

ID R35440 standard; protein; 170 AA.

AC R35440; (first entry)

DT 13-AUG-1993

DE Human basic myelin protein.

KW BMP; MS; multiple sclerosis; homologue; myelin basic protein; MBP.

OS Homo sapiens.

Key

Location/Qualifiers

FT peptide 61 . 106 /note= "neutralising fragment"
 FT peptide 1. . 15 /note= "neutralising fragment"
 FT peptide 4. . 18 /note= "neutralising fragment"
 FT peptide 9. . 23 /note= "neutralising fragment"
 FT peptide 15. . 35 /note= "neutralising fragment"
 FT peptide 20. . 37 /note= "neutralising fragment"
 FT peptide 31. . 46 /note= "neutralising fragment"
 FT modified-site 1 /note= "acetylated"

PD 29-APR-1993.
 PR 15-OCT-1992; CA0448.
 PR 22-OCT-1991; CA-053799.
 PA (CATZ) CATZ I.
 PA (WARR) WARREN K G.
 PI Catz I, Warren KG;
 DR WPI; 93-12422/18.

PT Homologous peptide analogues of human basic myelin protein - used for treating multiple sclerosis

PS Disclosure; Fig 4; 26pp; English.

CC The sequence is that of human basic myelin protein (BMP). Fragments of this sequence are claimed (see features) which are able to neutralise anti-BMP antibodies and are thus useful in treatment of multiple sclerosis. The fragments may be prod. synthetically and avoids the dangers associated with the use of the natural protein, e.g. transmission of neuroviruses. Also the peptides are too small to be immunogenic.

SQ Sequence 170 AA;

Query Match 98.6%; Score 909; DB 1; Length 170;
 Best Local Similarity 98.8%; Pred. No. 7.4e-89; Matches 168; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQKRPSQHSKYLATASTMDHARHGFLPKHRDTGILDSIGRFGGDRGAPRGSKDS 61
 1 ASQKRPSQHSKYLATASTMDHARHGFLPKHRDTGILDSIGRFGGDRGAPRGSKDS 60

QY 62 HRPARTAHYGSLLPKSHGRTODENPVHFFRNIVPRTPPPSQGKGRLSLSRFSGAEG 121
 1 HRPARTAHYGSLLPKSHGRTODENPVHFFRNIVPRTPPPSQGKGRLSLSRFSGAEG 120

Db 122 ORPGFGYGRASDYKSAHKGFKGVDQGTLSKIFKLGGRDSRSGPMARR 171
 Db 121 ORPGFGYGRASDYKSAHKGFKGVDQGTLSKIFKLGGRDSRSGPMARR 170

QY 63 W00399 standard; Protein: 197 AA.
 ID W00399 standard; Protein: 197 AA.
 AC W00399;
 DE 01-FEB-1997 (first entry)
 KW Human myelin basic protein (foetal isoform).
 OS Myelin basic protein; MBP; MBP+X2cys81; proteolipid protein; PLP;
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;
 T-lymphocyte; T-cell; anergy; apoptosis.
 OS Homo sapiens.

Key

Location/Qualifiers

FT region 60. . 85 /label= X2

FT misc-difference 81 /note= "exon 2-encoded region"

FT /note= "Cys-81 may be replaced by any standard amino acid, esp. an uncharged amino acid of mol.wt. below about 150, paric. Ser, in constructs of the invention"

FT WO9634622-A1.
 PD 07-NOV-1996.
 PR 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Lenardo MJ, Matis L, McFarland HR, Mueller EE, Mueller JP;
 PI Nye SH, Polfrey CM, Squinto SP, Wilkins JA;
 DR WPI; 96-50589850.

PT New human myelin basic protein and proteolipid protein variant(s) - used in the assessment, diagnosis and treatment of multiple sclerosis

PT Claim 1; Page 79-80; 156PP; English.

CC The native human 21.5 kDa foetal isoform (W00399) of myelin basic protein, MBP+X2cys81, includes an exon 2-encoded region (X2) that may contain an epitope involved in the pathogenesis of multiple sclerosis (MS), the X2 region is not found in the MBP of healthy adults. Recombinant MBP+X2, or variants modified to improve bacterial expression (see also W0507), can be produced in a large scale in bacterial hosts. They are useful for assaying T-cells for responsiveness to MBP epitopes and can be used as therapeutic agents that act by inducing T-cell responses, including anergy and apoptosis, as a means of treating MS.

SQ Sequence 197 AA;

Query Match 97.5%; Score 899; DB 1; Length 197;
 Best Local Similarity 86.8%; Pred. No. 1e-87; Matches 171; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MASQKRPSQHSKYLATASTMDHARHGFLPKHRDTGILDSIGRFGGDRGAPRGSG-- 58
 1 MASQKRPSQHSKYLATASTMDHARHGFLPKHRDTGILDSIGRFGGDRGAPRGSKV 60

Db 1 MASQKRPSQHSKYLATASTMDHARHGFLPKHRDTGILDSIGRFGGDRGAPRGSKV 60
 QY 59 -----KDSHPARTAHYGSLLPKSHGRTODENPVHFFRNIVPRTPPPSQGKGRLSLSRFSGAEG 120

Db 61 PWLKGRSPSPSHARSQPGCNMVKDSHPARTAHYGSLLPKSHGRTODENPVHFFRNIVPRTPPPSQGKGRLSLSRFSGAEG 121

QY 95 VTPRTPPPSQGKGRLSLSRFSGAEGQRGFGFGGRASDYKSAHKGFKGVDQGTLSKIFKLGGRDSRSGPMARR 154
 Db 121 VTPRTPPPSQGKGRLSLSRFSGAEGQRGFGFGGRASDYKSAHKGFKGVDQGTLSKIFKLGGRDSRSGPMARR 180

QY 155 FKLGRDSRSGPMARR 171
 Db 181 FKLGRDSRSGPMARR 197

RESULT 7 W06107
 ID W06107 standard; Protein: 203 AA.
 AC W06107;
 DT 01-FEB-1997 (first entry)

| | | | |
|-----------------------|---|--|---|
| DE | Foetal myelin basic protein MBP+X2Cys81/bact. | FT | /label= Hexa-histidine tag |
| KW | Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP; | FT | /note= "the hexa-histidine tag facilitates |
| KW | multiple sclerosis; autoimmune disease; diagnosis; therapy; | FT | purification of the recombinant protein |
| KW | T-lymphocyte; T-cell; anergy; apoptosis. | FT | from host cells" |
| OS | Synthetic. | PN | |
| FH | Key | Location/Qualifiers | |
| FT | region | 50..85 | /label= X2 |
| FT | | | /note= "exon 2-encoded region" |
| PN | W09634622-A1. | | |
| PD | 07-NOV-1996. | PD | 07-NOV-1996. |
| PF | 22-APR-1996; U05611. | PF | 02-APR-1996; U05611. |
| FT | | PR | 02-MAR-1995; US-431648. |
| FT | | PR | 02-MAY-1995; US-431644. |
| FT | | PR | 07-JUN-1995; US-482114. |
| PR | 01-JUN-1995; US-482114. | PA | (ALEX-) ALEXION PHARM INC. |
| PA | (USSH) US DEPT HEALTH & HUMAN SERVICES. | PA | (USSH) US DEPT HEALTH & HUMAN SERVICES. |
| PI | Lenard MJ, Matis L, McFarland HF, Mueller EE, Mueller JP; | PA | Lenard MJ, Matis L, McFarland HF, Mueller EE, Mueller JP; |
| PI | Nye SH, Peifrey CM, Squinto SP, Wilkins JA; | PI | Nye SH, Peifrey CM, Squinto SP, Wilkins JA; |
| DR | WPI; 96-50398/50. | DR | WPI; 96-50398/50. |
| PT | New human myelin basic protein and proteolipid protein variant(s) - | PT | New human myelin basic protein and proteolipid protein variant(s) - |
| PT | used in the assessment, diagnosis and treatment of multiple | PT | used in the assessment, diagnosis and treatment of multiple |
| PS | sclerosis | PS | sclerosis |
| CC | disclosure; Page 81-82; 156pp; English. | CC | disclosure; Page 82-83; 156pp; English. |
| CC | A 21.5 kDa foetal isoform (W06107) of myelin basic protein, | CC | A 21.5 kDa foetal isoform (W06108) of myelin basic protein (T41896) |
| CC | MBP+X2Cys81/bact. is the product of a DNA construct (T41896) | CC | MBP+X2Cys81/bact. is the product of a DNA construct (T41897) |
| CC | based on the human foetal MBP+X2Cys81 isoform (W00399) but | CC | based on the human foetal MBP+X2Cys81 isoform (W00399) but |
| CC | utilising bacterially-preferred codons in place of the native human | CC | utilising codons that are highly expressed in bacterial genes in |
| CC | cocones (see also T41897). This increases prodn. of the MBP in E. coli by at least 50%. | CC | place of the native codons (see also T41899) and incorporating a |
| CC | Recombinant MBP 21.5 polypeptides (see also W00399 and W06107) are | CC | sequence coding for a hexa-histidine tail. This allows large-scale prodn. and purification of the MBP in bacterial hosts. |
| CC | useful in the clinical assessment, diagnosis and treatment of MS. | CC | useful in the clinical assessment, diagnosis and treatment of MS. |
| SQ | Sequence 203 AA; | SQ | Sequence 203 AA; |
| Query Match | 97.5%; Score 899; DB 1; Length 203; | Query Match | 97.5%; Score 899; DB 1; Length 203; |
| Best Local Similarity | 86.8%; Pred. No. 1e-87; 0; Mismatches 171; Conservative 0; Indels 26; Gaps 1; | Best Local Similarity | 86.8%; Pred. No. 1e-87; 0; Mismatches 171; Conservative 0; Indels 26; Gaps 1; |
| Matches | | Matches | |
| 171; | | 171; | |
| 1 | MASQKRPQRHSKYLATASTMDHARHGFLPKHRDIGIILDSIGRFFGGDRGAKPKRGSG-- 58 | QY | 1 MASOKRPSQRHSKYLATASTMDHARHGFLPKHRDIGIILDSIGRFFGGDRGAKPKRGSG-- 58 |
| Db | 1 MASOKRPSQRHSKYLATASTMDHARHGFLPKHRDIGIILDSIGRFFGGDRGAKPKRGSGKV 60 | Db | 1 MASOKRPSQRHSKYLATASTMDHARHGFLPKHRDIGIILDSIGRFFGGDRGAKPKRGSGKV 60 |
| QY | 59 -----KDSHHPARTAHYGLSLPKQSHKGRTQDENPVVHFKNI 94 | QY | 59 -----KDSHHPARTAHYGLSLPKQSHKGRTQDENPVVHFKNI 94 |
| Db | 61 PWLKPGRSPLPASHRSQPGLCNMVKDSSHPARTAHYGLSLPKQSHKGRTQDENPVVHFKNI 120 | Db | 61 PWLKPGRSPLPASHRSQPGLCNMVKDSSHPARTAHYGLSLPKQSHKGRTQDENPVVHFKNI 120 |
| QY | 95 VTPRTTPPSQGKGRGLSLSREFSWGAEGORPGFGYGRASDYSAHKGFKGYDAQTLISKI 154 | QY | 95 VTPRTTPPSQGKGRGLSLSREFSWGAEGORPGFGYGRASDYSAHKGFKGYDAQTLISKI 154 |
| Db | 121 VTPRTTPPSQGKGRGLSLSREFSWGAEGORPGFGYGRASDYSAHKGFKGYDAQTLISKI 180 | Db | 121 VTPRTTPPSQGKGRGLSLSREFSWGAEGORPGFGYGRASDYSAHKGFKGYDAQTLISKI 180 |
| QY | 155 FKLGGDRSRSQSPMARR 171 | QY | 155 FKLGGDRSRSQSPMARR 171 |
| Db | 181 FKLGGDRSRSQSPMARR 197 | Db | 181 FKLGGDRSRSQSPMARR 197 |
| RESULT | 9 | RESULT | 9 |
| W06108 | ID W06103 standard; Protein: 373 AA. | W06103 | ID W06103 standard; Protein: 373 AA. |
| AC | W06103; | AC | W06103; |
| DT | 01-FEB-1997 (first entry) | DT | 01-FEB-1997 (first entry) |
| DE | MP4 chimera (MBP21.5-delta PLP4 fusion). | DE | MP4 chimera (MBP21.5-delta PLP4 fusion). |
| KW | Proteolipid protein; PLP; delta PLP; myelin basic protein; MBP; | KW | Proteolipid protein; PLP; delta PLP; myelin basic protein; MBP; |
| KW | MBP21.5; multiple sclerosis; autoimmune disease; diagnosis; | KW | MBP21.5; multiple sclerosis; autoimmune disease; diagnosis; |
| KW | therapy; T-lymphocyte; T-cell; anergy; apoptosis; MP3 chimera. | KW | therapy; T-lymphocyte; T-cell; anergy; apoptosis; MP3 chimera. |
| OS | Synthetic. | OS | Synthetic. |
| FH | Key | Location/Qualifiers | |
| FT | region | 60..85 | /label= X2 |
| FT | | /note= "exon 2-encoded region, with Cys81Ser | |
| FT | | mutation" | |
| FT | peptide | 198..200 | /label= Spacer |
| FT | | 201..373 | |
| FT | | 201..205 | /label= Delta_PLP4 |

/note= "synthetic N-terminal peptide not found in the native protein" PT
 region FT
 /label= Epitope PT
 /note= "PIP epitope associated with MS" DR
 210. .230 PR
 /label= Epitope used in the assessment, diagnosis and treatment of multiple
 region FT
 /note= "PIP epitope associated with MS" PR
 241. .261 PT
 /label= Epitope
 /note= "PIP epitope associated with MS" PS
 242. .259 Claim 34; Page 110-112; 156pp; English.
 /label= Epitope CC
 /note= "PIP epitope associated with MS" CC
 244. .257 MP4 chimera (WO103) is a fusion protein composed of human myelin basic protein (MBP) foetal isoform MBP21.5 (See also WO399) and delta PLP4 (W0501), a proteolipid protein (PLP) mutant that lacks all 4 hydrophobic domains of native human PLP (WO106), but includes PLP epitopes associated with multiple sclerosis (MS). It can be expressed in E. coli transformants using a DNA construct (T41893) contg. the MBP21.5-delta PLP4 gene fusion. MBP chimeras and other novel PLP/MBP21.5 polypeptides (WO399-400, WO6101-08) are useful for the clinical assessment, diagnosis and treatment of MS. CC
 region FT
 /note= "PIP epitope associated with MS" CC
 248. .269
 /label= Epitope CC
 /note= "PIP epitope associated with MS" CC
 256. .269
 /label= Epitope SQ
 /note= "PIP epitope associated with MS" Sequence 373 AA;
 257. .269
 /label= Epitope
 /note= "PIP epitope associated with MS" QY
 268. .281
 /label= Epitope Db
 /note= "PIP epitope associated with MS" 1 MASOKRPSQRIGSKYLTASTMDHARHGFEPRHRGTLIDPSIGRFGGDGAKRGSG- 58
 270. .303 QY
 /label= Epitope 1 MASOKRPSQRIGSKYLTASTMDHARHGFEPRHRGTLIDPSIGRFGGDGAKRGSKV 60
 /note= "PIP epitope associated with MS" 59 .----- KDSHHPTARTAHYGSQPKSHRTQDENDPVWHFKNI 94
 region FT
 /note= "PIP epitope associated with MS" 61 PWLKPGRSPRLPSHARSQPGLCCNMVKDSSHHPARTAHYGSQPKSHRTQDENDPVWHFKNI 120
 292. .304
 /label= Epitope
 /note= "PIP epitope associated with MS" QY
 95 VTPRITPPSQQKGKRGISLSRSRSGWAGQRGFGYGRASDKISKAHKGFKVDAQTLISKI 154
 region FT
 /note= "PIP epitope associated with MS" Db
 295. .306 121 VTPRITPPSQQKGKRGISLSRSRSGWAGQRGFGYGRASDKISKAHKGFKVDAQTLISKI 180
 /label= Epitope
 /note= "PIP epitope associated with MS" QY
 314. .326 155 VKLGRDRSRSSPMARR 171
 /note= "PIP epitope associated with MS" Db
 314. .326 181 VKLGRDRSRSSPMARR 197
 /label= Epitope
 /note= "PIP epitope associated with MS" RESULT 10
 region FT
 /note= "PIP epitope associated with MS" WD6102
 326. .337 ID W05102 standard: Protein; 385 AA.
 /label= Epitope AC W06102;
 /note= "PIP epitope associated with MS" DT 01-FEB-1997 (first entry)
 339 DE MB21.5-delta PLP3 fusion.
 /label= Epitope KW Proteolipid Protein; PLP; delta PLP3; myelin basic protein; MBP;
 /note= "PIP epitope associated with MS" KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
 region FT KW therapy; T-lymphocyte; T-cell; anergy; apoptosis; MP3 chimera.
 /note= "PIP epitope associated with MS" OS Synthetic.
 region FT FH Key
 /note= "PIP epitope associated with MS" domain Location/Qualifiers
 213. .234 1.197
 /label= Epitope FT peptide
 /note= "encephalitogenic epitope in mouse model" 198. .200
 256. .269 /label= MBP21.5
 /label= Epitope FT peptide
 /note= "encephalitogenic epitope in mouse model" 201. .385
 region FT domain /label= Spacer
 292. .304
 /label= Epitope PN W09634622-A1.
 /note= "encephalitogenic epitope in mouse model" PD 07-NOV-1996.
 369. .373 PF 22-APR-1996; WO5611.
 peptide FT PR 02-MAY-1995; US-431648.
 /note= "hexa-histidine-tag PR 02-MAY-1995; US-431644.
 protein purification" PR 07-JUN-1995; US-482114.
 protein purification" PR (ALEX-) ALEXION PHARM INC.
 peptide PR (USSA) US DEPT HEALTH & HUMAN SERVICES.
 /note= "hexa-histidine-tag PR Lenardo MJ, Matlis L, Marland HF, Mueller EE, Mueller JP;
 protein purification" PR Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 protein purification" DR WPI; 96-505898/50.
 peptide PR N-PSDB; T41892.
 peptide PR New human myelin basic protein and proteolipid protein variant(s) -
 peptide PR PA (ALEX-) ALEXION PHARM INC.
 peptide PR PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 peptide PR DR WPI; 96-505898/50.
 peptide PR N-PSDB; T41892.
 peptide PR New human myelin basic protein and proteolipid protein variant(s) -

PT used in the assessment, diagnosis and treatment of multiple sclerosis

PT MP3 chimera (W05105) is a fusion protein composed of human myelin basic protein (MBP) foetal isoform MBP21.5 (see also W00390) and delta PLP (W00400), a proteolipid protein (PLP) muetin that lacks hydrophobic domains 1, 3 and 4 of native human PLP (W05105) but includes PLP epitopes associated with multiple sclerosis (MS). It can be expressed in E. coli transformants using a DNA construct (T41892) contg. the MBP21.5-delta PLP3 gene fusion. MP3 chimera and other novel PLP/MBP21.5 polypeptides (W00399-400, W05101-08) are useful for the clinical assessment, diagnosis and treatment of MS.

SQ Sequence 385 AA:

Query Match 97.5%; score 899; DB 1; length 385;

Best Local Similarity 86.8%; Pred. No. 2, 3e-87; Matches 0; Mismatches 171; Conservative 0; Indels 26; Gaps 1;

QY 1 MASQRSPQRGSKYKLAATSTMHDHARHGFLPRHRRTGILDSIGRFFGDKAPRKGS-- 58

Db 1 MASQRSPQRGSKYKLAATSTMHDHARHGFLPRHRRTGILDSIGRFFGDKAPRKGSKV 60

QY 59 -----FDSHHPARTAHYGSLPKQSKHGTODENPVVHFKNI 94

Db 61 PWLKGPGRSPLPSHARSQPGLCNMYKDHSHHPARTAHYGSLPKQSKHGTODENPVVHFKNI 120

QY 95 VTPRPPPSQGKGRLSLSRFSGWAEQGRQFGFGGGRASDYSKSAHKGFKVDAQGTLISKI 154

Db 121 VTPRTPPPSQQGKGRLSLSRFSGWAEQGRQFGFGYGRASDYSKSAHKGFKVDAQGTLISKI 180

QY 155 FKLGGDRSRSQGPMMAR 171

Db 181 FKLGGDRSRSQGPMMAR 197

RESULT 11

ID W06105 standard; Protein: 492 AA.

AC W06105; standard; Protein: 492 AA.

DT 01-FEB-1997 (first entry)

DE MNOP4 chimera (MBP21.5-MOG-delta PLP4 fusion).

KW Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP; MBP21.5; multiple sclerosis; autoimmune disease; diagnosis; therapy; T-lymphocyte; T-cell; MNOP4 chimera;

KW myelin oligodendrocyte glycoprotein; MOG.

OS Synthetic.

FT Location/Qualifiers

FT Key

FT protein 1. 487

FT /note= "preferred protein of the invention"

FT domain 1. 197

FT /label= MBP21.5

FT domain 198. -319

FT /label= MOG

FT /note= "MOG extracellular domain"

FT domain 320. -486

FT /label= Delta-PLP4

FT region 327. -338

FT /label= PLP epitope

FT /note= "PLP epitope associated with MS"

FT region 329. -349

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 360. -380

FT /label= PLP epitope

FT /note= "PLP epitope associated with MS"

FT region 361. -278

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 363. -376

FT /label= PLP epitope associated with MS"

FT /note= "PLP epitope associated with MS"

FT --- .

FT region 357. -378

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 375. -388

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 376. -388

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 387. -400

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 389. -402

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 411. -423

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 411. -426

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 414. -425

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 443. -445

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 445. -456

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 445. -458

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 470. -484

FT /label= Epitope

FT /note= "PLP epitope associated with MS"

FT region 332. -353

FT /label= Epitope

FT /note= encephalitogenic epitope in mouse model

FT region 375. -388

FT /label= Epitope

FT region 411. -423

FT /label= Epitope

FT /note= encephalitogenic epitope in mouse model

FT peptide 487. -492

FT /label= Histidine-tag

FT /note= "hexa-histidine tag facilitates recombinant protein purification"

FT PN WO9534622-A1.

FT PD 07-NOV-1996.

FT PR 07-NOV-1996; U05611.

FT PR 22-APR-1996; U05611.

FT PR 02-MAY-1995; US-431648.

PR 02-MAY-1995; US-431644.

PR 07-JUN-1995; US-482114.

PA (ALEX) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP; Nye SH, Pelfrey CM, Squinto SP, Wilkins JA; DR NPI; DR N-PSDB; T41895.

PT New human myelin basic protein and proteolipid protein variant(s) - used in the assessment, diagnosis and treatment of multiple sclerosis

PT Claim 36: Page 115-117; 156pp; English.

PT Label 36: Page 115-117; 156pp; English.

CC MNOP4 chimera (W05105) is a fusion protein composed of human myelin basic protein (MBP) foetal isoform MBP21.5 (see also W00399), the extracellular domain of human myelin oligodendrocyte glycoprotein (MOG) and delta PLP4 (W06101), a proteolipid protein (PLP) muetin. MBP21.5, PLP and MOG are all recognised by autoreactive T cells from multiple sclerosis (MS) patients. The chimera was produced using a DNA construct (T41895) obtgd. by inserting a sequence encoding the MOG moiety into MP4 chimera DNA (see also T41893). MNOP4 chimera

can be expressed in bacterial cell hosts. PLP and MBP polypeptides (see also WO2010/04, WO2010/08) are useful in the clinical assessment, diagnosis and treatment of MS.

| Key | location/Qualifiers |
|-----------------------|---|
| QY | 2 ASQRPSORHGSKYLATASTMDHARHGFLPRHRDGILDSIGRFFGGDGRAPKGSGKSGSKS 1 |
| Db | 174 ASQRPSORHGSKYLATASTMDHARHGFLPRHRDGILDSIGRFFGGDGRAPKGSGKVP 233 |
| QY | 59 ----- 1-----KDHARTAHGSLPSOKSHGRTQDENPVWIFKNIV 95 |
| Db | 234 WLPGRSPLPSHARSQPGCJNMYKDHHARTAHGSLPSOKSHGRTQDENPVWIFKNIV 293 |
| QY | 96 TPRIPPPSGKGRGLSLSHPSWGAEGQRGFGYGRASDYSKAHKGFKGYDAQGTLISKIF 155 |
| Db | 294 TPRIPPPSGKGRGLSLSRFSWGAEGQRGFGYGRASDYSKAHKGFKGYDAQGTLISKIF 353 |
| QY | 156 KLGDRDSSGSPMARR 171 |
| Db | 354 KLGDRDSSGSPMARR 369 |
| RESULT | 13 |
| R30736 | R30736 standard; Protein; 170 AA. |
| ID | R30736; |
| AC | R30736; |
| DT | 21-MAY-1993 (first entry) |
| DE | Human MBP. |
| KW | Acetylcholine receptor; MHC; myelin basic protein; MBP. |
| OS | Synthetic. |
| FH | Key |
| FT | Location/Qualifiers |
| modified_site | 1 /note= "N-Ac-Ala" |
| FT | modified_site 107 /note= "Me-Arg" |
| FT | peptide 1. 14 "claim 30; page 68" |
| FT | note= "claim 30; page 68" |
| PN | W0218150-A. |
| PD | 29-OCT-1992. |
| PF | 23-APR-1992; US03391. |
| PR | 23-APR-1991; US-698840. |
| PA | (ANER-) ANERGEN INC. |
| PI | Clark BR, Leitch BL, Sharma SD; |
| DR | WPI: 93-03605-04. |
| PT | Pure major MHC-peptide complex - useful in treating deleterious immune response such as auto-immunity |
| PT | Claim 30: Page 68 + Fig 7; 93pp; English. |
| PS | A method is claimed for the prepn. of a pure major MHC-peptide complex. The MHC component is a Class II glycoprotein of the MHC and the peptide comprises amino acids 1-14 of MBP. |
| CC | Sequence 170 AA; |
| SQ | Sequence 170 AA; |
| Query Match | 96.6%; Score 891; DB 1; Length 170; |
| Best Local Similarity | 98.2%; Pred. No. 5. ge-8/ 3; Indels 0; Gaps 0; |
| Matches | 167; Conservative 0; Mismatches 0; Gaps 0; |
| QY | 2 ASQRPSORHGSKYLATASTMDHARHGFLPRHRDGILDSIGRFFGGDGRAPKGSGKDS 61 |
| Db | 1 ASQRPSORHGSKYLATASTMDHARHGFLPRHRDGILDSIGRFFGGDGRAPKGSGKDS 60 |
| QY | 62 HHPARTAHGSLPSOKSHGRTQDENPVWIFKNIVTPRIPPPSGKGRGLSLSRFSWGAEG 121 |
| Db | 61 HHAARTAHGSLPSOKSHGRTQDENPVWIFKNIVTPRIPPPSGKGRGLSLSRFSWGAEG 120 |
| QY | 122 QRPGEFYGRASDYSKAHKGFKGYDAQGTLISKIFKLGGDRSRSGSPMARR 171 |
| Db | 119 QRPGEFYGRASDYSKAHKGFKGYDAQGTLISKIFKLGGDRSRSGSPMARR 168 |
| RESULT | 15 |
| R48594 | R48594 standard; protein; 168 AA. |
| ID | R48594; |
| AC | R48594; |
| DT | 31-JUL-1994 (first entry) |
| DE | Rabbit myelin basic protein. |
| KW | Protein; myelin basic protein; retrovirus; neurological disease; by-stander antigen; TGF-beta; transforming growth factor-beta; T-cell; T-lymphocyte; myopathy; paraparesis; human immunodeficiency virus type 1; orcyctolagus cuniculus. |
| OS | Sequence 168 AA. |
| PN | WO404121-A. |
| DD | 01-MAR-1994. |
| PF | 17-AUG-1993; US-931217. |
| PR | 17-AUG-1992; US-931217. |
| PA | (AUTO-) AUTOIMMUNE INC. |
| PI | Haller DA, Weiner HL; |
| DR | WPI: 94-082786/10. |
| PT | Treating retroviral associated neurological disease - by admin. of by-stander antigen, causing release of transforming growth factor beta from suppressor T cells |
| PT | Disclosure; Page 49; 64pp; English. |
| PS | Myelin basic proteins (sequences R48592-96) and cattle proteolipid |
| RESULT | 14 |
| RO417 | RO417 standard; protein; 168 AA. |
| AC | RO417; |
| DE | Empirically determined sequence of myelin basic protein (MBP) |
| KW | Myelin basic protein; multiple sclerosis; autoantigen; autoimmune disease; autoimmunity; myelin sheath. |
| QY | ----- 1-----KDHARTAHGSLPSOKSHGRTQDENPVWIFKNIV 95 |
| Db | 121 QRPGFYGRASDYSKAHKGFKGYDAQGTLISKIFKLGGDRSRSGSPMARR 170 |

CC protein (R48592) elicit the release of TGF-beta from suppressor T-cells and target the T-cells to neural tissue under cytotoxic attack, thereby reducing neurological disease, e.g. HIV-1 associated myopathy, tropical spastic paraparesis and HIV infection.
CC
CC
CC
SQ Sequence 168 AA;

Query Match 90.2%; Score 832; DB 1; Length 168;
Best Local Similarity 91.2%; Pred. No. 1e-80; Matches 155; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
Matches 155; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
QY 2 ASQRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRFGGDRGAPRKGSKDS 61
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 ASQRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRFSSDRGAPRKGSKD- 59
QY 62 HHPRTARYHSLSLCKSHGTQDEPWPWFKNTVPRPPPSGKGCRDLISLSFSGAEG 121
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 -HAARTHYGLSPKSKHGRPODENPVVHFKNTVPRTPPSGKGCRGTVLSRFSWGAEG 118
QY 122 QRGFGYGRASDYKSAHGFKGDAQTLISKFKLGGDRSRSGPMMARR 171
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 QKFGFGYGRAGAKYKSAHGLKQDAGPLSRKLGDRDSNSGPMMARR 168

Search completed: September 26, 2000, 19:25:03
Job time: 5855 sec

